

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:15:36 ; Search time 33.5 Seconds
(without alignments)
1256.931 Million cell updates/sec

Title: US-09-787-126-4

Perfect score: 1675

Sequence: 1 MRRASRDYKYLSSSEMGs.....LLDPDQDNYFGAFKVDID 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	19 AAW83194	Human osteoprotegerin
2	1675	100.0	316	19 AAW83017	Osteoclastogenesis
3	1675	100.0	316	19 AAW59654	Amino acid sequenc
4	1675	100.0	316	20 AAY17874	Murine TRANCE. Mu
5	1675	100.0	316	21 AAY91024	Mouse OBM protein
6	1675	100.0	316	21 AAY84418	Amino acid sequenc
7	1675	100.0	316	21 AAY84419	Amino acid sequenc
8	1675	100.0	316	21 AAY78289	Mouse TRANCE prote
9	1597	95.3	318	22 AAB82092	Rat osteoclast dif
10	1554	92.8	294	19 AAW69956	NF-kB receptor act

11	1554	92.8	294	19 AAW68292	NF-kB receptor act
12	1554	92.8	294	22 AAE08737	Murine receptor ac
13	1554	92.8	294	22 AAE04425	Murine receptor ac
14	1554	92.8	294	22 AAE01992	Murine RANKL (re
15	1417.5	84.6	317	19 AAW83195	Human osteoprotege
16	1417.5	84.6	317	19 AAW69957	NF-kB receptor act
17	1417.5	84.6	317	19 AAW68293	NF-kB receptor act
18	1417.5	84.6	317	21 AAY84417	Amino acid sequenc
19	1417.5	84.6	317	22 AAE08738	Human receptor act
20	1417.5	84.6	317	22 AAE04426	Human receptor act
21	1417.5	84.6	317	22 AAE01993	Human full-length
22	1417.5	84.6	317	23 ABB08134	Human RANKL poly
23	1417.5	84.6	317	23 AAY78285	Human TRANCE prote
24	1409.5	84.1	317	19 AAW83018	Osteoclastogenesis
25	1318	78.7	501	22 AAB84420	Amino acid sequenc
26	1297	77.4	244	19 AAW83019	A murine OCIF-bind
27	1107	66.1	246	19 AAW83020	Osteoclastogenesis
28	1101	65.7	245	20 AAY17873	Human TRANCE. Hom
29	1100	65.7	244	23 AAY86148	Human PRO206 polyp
30	1100	65.7	244	23 AAY78286	Human TRANCE prote
31	960	57.3	409	23 AAO17115	GlutathioneStransf
32	960	57.3	409	23 AAW49711	Murine GSI-modf fu
33	855	51.0	160	21 AAB08272	Amino acid sequenc
34	852	50.9	173	21 AAY84421	Amino acid sequenc
35	852	50.9	187	21 AAY84420	Amino acid sequenc
36	842	50.3	173	21 AAY84422	A murine osteoprot
37	830	49.6	170	22 AAY08386	Mouse FLAG-murine
38	804.5	48.0	188	21 AAY84423	An osteoprotegerin
39	794.5	47.4	182	21 AAY84424	An osteoprotegerin
40	771	46.0	173	21 AAY84425	DNA encoding osteo
41	768	45.9	160	21 AAB08273	Amino acid sequenc
42	746	44.5	139	21 AAY91023	Mouse OBM protein
43	741	44.2	152	22 AAB67248	Human RANKL. Homo
44	732	43.7	173	21 AAY84426	An osteoprotegerin
45	387	23.1	74	21 AAY91020	Mouse OBM protein

ALIGNMENTS

RESULT 1

AAW83194

ID AAW83194 standard; Protein; 316 AA.

AC AAW83194;

DT 11-FEB-1999 (first entry)

DE Human osteoprotegerin binding protein from the 32D-F3 ins.

Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAH; hypercalcaemia; osteoclast differentiation and activation receptor; Paget's disease.

OS Homo sapiens.

XX W09846751-A1.

XX 22-OCT-1998.

PD 15-APR-1998; 98WO-US07584.

PR 30-MAR-1998; 98US-0052521.

PR 16-APR-1997; 97US-0842842.

PR 23-JUN-1997; 97US-0880855.

XX (AMGE-) AMGEN INC.

XX Boyle WJ;

PI WPI; 1998-594578/50.

DR N-PSDB; AAV70284.

RESULT 2	
AAW83017	
ID	AAW83017 standard; Protein; 316 AA.
XX	
XX	
AC	AAW83017;
XX	
DT	10-FEB-1999 (first entry)
XX	
DE	Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
XX	
KW	Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
KW	osteoclast; bone absorption factor; bone disorder; calcium metabolism.
XX	
OS	Unidentified.
XX	

Query Match	100.0%	Score 1675;	DB 19;	Length 316;
Best Local Similarity	100.0%;	Prod. No. 2.6e-143;		
Matches 316;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MRRASDYGKYLRSSEEMSGPGVPHCGPLHPASAPAPAPPAAASRSMFLALGLGIGQ	60	
Db	1	MRRASDYGKYLRSSEEMSGPGVPHCGPLHPASAPAPAPPAAASRSMFLALGLGIGQ	60	
Qy	61	VVCSIALFLYFRAQMDPNRISEDSHTCFYRILRLHENAGLQDSTLESEDITLPDSCRRMQ	120	
Db	61	VVCSIALFLYFRAQMDPNRISEDSHTCFYRILRLHENAGLQDSTLESEDITLPDSCRRMQ	120	
Qy	121	AFQGAQVQKELQHTVGPQFSGAPAMMGESLVDVAQRGKPEAQPPAHITINAAISPSGSHK	180	
Db	121	AFQGAQVQKELQHTVGPQFSGAPAMMGESLVDVAQRGKPEAQPPAHITINAAISPSGSHK	180	
Qy	181	VTLSWYHDRGWAKISNNLTSLNGKLRVNODGFYLYANICPRRHETSGSVPTDYQLMWY	240	
Db	181	VTLSWYHDRGWAKISNNLTSLNGKLRVNODGFYLYANICPRRHETSGSVPTDYQLMWY	240	
Qy	241	VVKTSIKTIPSSHNLKMGGSTNWSGNSFEHYISINVGGFFKLRAGEISISIQVSNPSLLDP	300	
Db	241	VVKTSIKTIPSSHNLKMGGSTNWSGNSFEHYISINVGGFFKLRAGEISISIQVSNPSLLDP	300	
Qy	301	DQDATYFGAFKVVQDID	316	
Db	301	DQDATYFGAFKVVQDID	316	

RESULT 3

AAW59654
ID AAW59654 standard; Protein; 316 AA.

XX AC AAW59654;

XX DT 24-SEP-1998 (first entry)

XX DE Amino acid sequence of mouse 499E9 protein.

XX KW Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
XX KW antagonist; autoimmune disorder; rheumatoid arthritis;
XX KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
XX KW acute inflammatory response; antibody; antigen; cancer.

XX OS Mus sp.

XX FH Location/Qualifiers

XX DT 1..49

XX FT Domain /note= "intracellular domain"

XX FT 70..316

XX FT Domain /note= "extracellular domain"

XX PN W09825958-A2.

XX PD 18-JUN-1998.

XX PF 12-DEC-1997; 97WO-US22766.

XX PR 13-DEC-1996; 96US-0032846.

XX FA (SCHE) SCHERING CORP.

XX FH Gorman DM, Mattson JD;

XX DR WPI: 1998-348452/30.

XX DR N-PSDB: AAW41489.

XX FT Mouse cell surface antigen, 499E9 protein - used to treat conditions
XX FT associated with abnormal physiology or development

XX PS Claim 1; Pages 8-11; 59pp; English.

XX CC This is the amino acid sequence of the mouse 499E9 protein, used
XX CC in the method of the invention to treat conditions associated with
XX CC abnormal physiology or development. The 499E9 protein is expressed
XX CC highly on polarised Th1 T cells, binding of 499E9 to its receptor may
XX CC result in either immune cell expansion or apoptosis. Antagonists of
XX CC 499E9 may be used to modulate immune responses in abnormal situations,
XX CC e.g. autoimmune disorders including rheumatoid arthritis, systemic
XX CC lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
XX CC acute inflammatory responses in which T-cell expansion, activation or
XX CC immunological T-cell memory play an important role. The antibodies
XX CC can be used to raise anti-idiotypic antibodies which will be useful
XX CC in detecting or diagnosing various immunological conditions related to
XX CC the expression of antigens of 499E9. The antibodies, and fragments of
XX CC 499E9 can be used in the treatment of conditions associated with
XX CC abnormal physiology or development, including abnormal proliferation
XX CC (e.g. cancerous conditions) or degenerative conditions.

XX SQ Sequence 316 AA;

Query Match 100.0%; Score 1675; DB 19; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.6e-143;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRASRDYGYKLRSEFGSGVPHGPHLPAPCAPAPPAPPAASRSMFALLGLGIGQ 60

DB 1 MRASRDYGYKLRSEFGSGVPHGPHLPAPCAPAPPAPPAASRSMFALLGLGIGQ 60

QY 61 VVCSTALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120

DB 61 VVCSTALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120

QY 121 AFOGAVOKELQHLVGPORFSGAPAMMEGSLDVAORCKPEAOPFAHLTINAAISPSGSHK 180
DB 121 AFOGAVOKELQHLVGPORFSGAPAMMEGSLDVAORCKPEAOPFAHLTINAAISPSGSHK 180
QY 181 VTLSWYHDRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLQLMVY 240
DB 181 VTLSWYHDRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLQLMVY 240
QY 241 VVTSIKIPSSHNLMKGGSTKNMSEFHFYSINVGGFKLKLRAGEISIQVSNPSLLDP 300
DB 241 VVTSIKIPSSHNLMKGGSTKNMSEFHFYSINVGGFKLKLRAGEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVDID 316
DB 301 DQDATYFGAFKVDID 316

RESULT 4

AAV17874

ID AAV17874 standard; Protein; 316 AA.

XX AC AAV17874;

XX DT 17-AUG-1999 (first entry)

XX DE Murine TRANCE.

XX KW TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
XX KW TNF-related activation induced cytokine; Immune response; cancer;
XX KW autoimmune disease; HIV; hypersensitivity; allergen.

XX OS Mus musculus.

XX PN W09929865-A2.

XX PD 17-JUN-1999.

XX PF 14-DEC-1998; 98WO-US26486.

XX PR 11-DEC-1998; 98US-0989479.

XX PR 12-DEC-1997; 97US-0989479.

XX PR 03-MAR-1998; 98US-0034099.

XX FA (UYRQ) UNIV ROCKEFELLER.

XX FH Choi Y, Josien R, Steinman R, Won B;

XX DR WPI: 1999-385609/32.

XX DR N-PSDB: AAX80224.

XX FT TNF like proteins for treating autoimmunity and cancer

XX PS Claim 9; Fig 3; 164pp; English.

XX CC The present sequence represents murine TRANCE-related activation induced
XX CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their
XX CC variants, fragments, derivatives or analogues may be used as modulators
XX CC of immune response in a mammal comprising, antisense sequences to
XX CC TRANCE and fusion proteins comprising human and/or murine TRANCE.
XX CC Agonists and antagonists of TRANCE, can be used to modulate immune
XX CC response by increasing or decreasing the life span of mature dendritic
XX CC cells and increasing or decreasing T cell activation. These techniques
XX CC are especially useful for treating immune system related conditions such
XX CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
XX CC The TRANCE polypeptides can be used to increase the viability of
XX CC dendritic cells in vivo or in vitro, especially when used in conjunction
XX CC with proteins of the tumour necrosis factor (TNF) superfamily (especially
XX CC CD40L or TNF-alpha).

XX SQ Sequence 316 AA;

Query Match 100.0%; Score 1675; DB 20; Length 316;

XX
PA
(MEBI-) M & E BIOTECH AS.

[illegible]

11

Qy	23	GVPHGPHLPAPSA	PAPAPPPAASRSMFLALLGLGQVVCSTALFLYFRAQMDPNRISE	82
Db	1	GVPHGPHLPAPSA	PAPAPPPAASRSMFLALLGLGQVVCSTALFLYFRAQMDPNRISE	60
Qy	83	DSTHCFYRIILRHENAGLQDSTLESEDTLPDSCRRMKAFQGVOKELQHIVGPQFSGA	1424	
Db	61	DSTHCFYRIILRHENADLQDSTLESEDTLPDSCRRMKAFQGVOKELQHIVGPQFSGA	120	
Qy	143	PAMMEGSWLDVAORGRKEAPDPPFAHLTNAASIPSGSHKVTLSWYHDRGWAKLSNMTLSN	202	
Db	121	PAMMEGSWLDVAORGRKEAPDPPFAHLTNAASIPSGSHKVTLSWYHDRGWAKLSNMTLSN	180	
Qy	203	GKLRVNDGFFYLYIANICFRHHETSGSVPTDYIQLVMVYVKTTSIKIPSSHNLKMGGSTKN	262	
Db	181	GKLRVNDGFFYLYIANICFRHHETSGSVPTDYIQLVMVYVKTTSIKIPSSHNLKMGGSTKN	240	

QY 263 WSGNSEPHFYSINVGPFKLRAGEEISIQVSNPSLLDPDQDATYGAFAKVDID 316
 Db 241 WSGNSEPHFYSINVGPFKLRAGEEISIQVSNPSLLDPDQDATYGAFAKVDID 294

RESULT 13
 AAE04425
 ID AAE04425 standard; Protein; 294 AA.
 XX AC AAE04425;
 XX DT 04-SEP-2001 (first entry)
 XX DE Murine receptor activator of NF- χ 1 B ligand (RANKL) protein.
 XX KW Murine; receptor activator of NF- χ 1 B; RANK; tumour necrosis factor;
 KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF;
 W chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.
 JS Mus musculus.

XX Key Location/Qualifiers
 FH Region 139..294
 FT /note="Receptor binding region"
 XX US6242213-B1.
 XX 05-JUN-2001.
 XX 22-DEC-1997; 97US-0995659.
 XX 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0077181.
 PR 14-OCT-1997; 97US-0064671.
 XX (IMMV) IMMUNEX CORP.
 XX Anderson DM;
 XX WPI; 2001-407216/43.
 DR N-PSDB; AAD08714.
 XX New DNA molecules, useful for producing ligands (which are useful for
 PT regulating immune response and in screening for inhibitors of NF- χ 1 B
 PT receptor activator) of the receptor activator of NF- χ 1 B (RANK)
 XX Example 7; Column 59-62; 43pp; English.

CC The present invention relates to receptor activator of NF- χ 1 B (RANK)
 CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
 CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
 CC proteins respectively. RANK is a member of the tumour necrosis factor
 CC (TNF) superfamily and it closely resembles CD40 in the extracellular
 CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
 CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
 CC The ligands are useful for regulating immune response and in screening
 CC for inhibitors of RANK. The present sequence is murine RANKL protein.
 XX Sequence 294 AA;

Query Match 92.88; Score 1554; DB 22; Length 294;
 Best Local Similarity 99.78; Pred. No. 2.1e-132;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 23 GVPHEGPHAPAPAPAPPAASRSMFLALIGLIGVGWCSIALFLYFRAQMDPNRISE 82
 Db 1 GVPHEGPHAPAPAPAPPAASRSMFLALIGLIGVGWCSIALFLYFRAQMDPNRISE 60
 QY 83 DSTHCFYRILRHENAGLDSTLESDTLDPSCRMKQAFQVQKELQHLIVGPQRFSGA 142
 Db 61 DSTHCFYRILRHENAGLDSTLESDTLDPSCRMKQAFQVQKELQHLIVGPQRFSGA 120

QY 143 PAMGEGSWLDVAQKPEAOPFAHLITNAASIPSGSHKVTLSWYHDSGAKISNMTLSN 202
 Db 121 PAMGEGSWLDVAQKPEAOPFAHLITNAASIPSGSHKVTLSWYHDSGAKISNMTLSN 180
 QY 203 GKLRVNDGFFYLYANICFRHETSGSVPTDYQLQMLVYVTKTSIKIPSSHNLKMGSGTKN 262
 Db 181 GKLRVNDGFFYLYANICFRHETSGSVPTDYQLQMLVYVTKTSIKIPSSHNLKMGSGTKN 240
 QY 263 WSGNSEPHFYSINVGPFKLRAGEEISIQVSNPSLLDPDQDATYGAFAKVDID 316
 Db 241 WSGNSEPHFYSINVGPFKLRAGEEISIQVSNPSLLDPDQDATYGAFAKVDID 294

RESULT 14
 AAE01992
 ID AAE01992 standard; Protein; 294 AA.
 XX AC AAE01992;
 XX DT 31-JUL-2001 (first entry)
 XX DE Murine RANKL (receptor activator of NF-kappaB ligand) protein.
 XX KW Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;
 KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KW immune system dysfunction; familial expansile osteolysis; FEO;
 KW early onset Paget's disease of bone; EP; cytostatic.
 XX Mus musculus.
 XX WO200136637-A1.
 XX 25-MAY-2001.
 XX 14-NOV-2000; 2000WO-US31459.
 XX 17-NOV-1999; 99US-0442029.
 XX (IMMV) IMMUNEX CORP.
 XX Anderson DM, Hughes AE;
 XX WPI; 2001-329222/34.
 DR N-PSDB; AAD05903.
 XX New DNA encoding a receptor activator of NF-kappaB polypeptide for the
 PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
 PT Disclosure; Page 74-75; 96pp; English.

CC The present invention relates to a novel receptor, referred to as RANK
 CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
 CC (tumour necrosis factor) receptor superfamily. RANK is a type I
 CC transmembrane protein that interacts with TNF receptor-associated
 CC factors (TRAFs). Triggering of RANK by overexpression or co-expression
 CC of the transcription factor NF-kappaB, a ubiquitous transcription factor
 CC that is most extensively utilised in cells of the immune system.
 CC Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating
 CC negative effects of inflammatory reactions, and the effects of excess
 CC bone resorption. The RANK DNAs, proteins and their analogues are useful
 CC for the preparation of pharmaceutical compositions, for infecting target
 CC cells for use in gene therapy applications in diagnosing diseases
 CC associated with RANK, and as targets for use in screening assays. They
 CC may be used in the treatment or diagnosis of immune system dysfunction.
 CC The present invention also encompasses gene therapy methods to correct
 CC gene-activating mutations, associated with e.g. familial expansile
 CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
 CC present amino acid sequence is murine RANKL (muRANKL) protein.
 XX Sequence 294 AA;

The present sequence is human osteoprotegerin (OPG) binding protein. CC
CC host cells transfected with vectors containing nucleic acid molecules CC
CC encoding OPG binding protein are used to produce recombinant OPG binding CC
CC protein. OPG binding protein is used in binding assays to determine CC
CC osteoprotegerin (OPG) in biological samples; to screen for specific CC
CC binding agents (particularly agonists and antagonists, including CC
CC intracellular proteins); to raise Ab (useful in immunoassays for CC

Search completed: April 16, 2003, 12:18:35
Job time : 35.5 secs

A; Accession: A49266

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: GB:U03470; NID:G440178; PIDN:AAC52129.1; PID:G440179
C;Keywords: glycoprotein; transmembrane protein

Query Match 10.9%; Score 183; DB 2; Length 278;
Best Local Similarity 23.4%; Pred. No. 9.5e-08;
Matches 75; Conservative 42; Mismatches 107; Indels 96; Gaps 13;

QY 14 SSEEMSG-----PGVPHEGLHPAPSAPAPP-----PAASRSMFLALL 54
DB 34 SSGPRGQRRPPPPPPSPL-PPSPQPLPLPLKKNIELWLVFFPMVLVALV 92
QY 55 GLIGQVVCVIALFLYRAQMDNRISEDTHCFYRILRLHENAGLDQSTLESEDITLPS 114
DB 93 GMGLG-----MYQLFHLQKELAELEFTH-----SLRVSSFEKQIANPST 133
QY 115 CRMKQAFQAVOKELQHIIVGPORFSGAPAMGSMGLDVAQRKPEAQPPAHLTIN--AA 172
DB 134 PSETK-----KPRS--VAHLTGPNRSR 153
QY 173 SIPSGSHKVTLSWYHGRGAKISNMTLSNGLRVNODGFFYLYANICFRHHETSGSVPT 232
DB 154 SIP-----LEWEDTYGTALISGVKRYKGLVINEAGLYFYYSKYPR-GQSCNSQP- 203
QY 233 DYQLQVMYVVKTSIKIPSSHNLMKGGSTKNWGNSEPHFYSINVGFFKLRAGEEISIOV 292
DB 204 --LSHKVYM--RNFKPGDVLVME-EKRLNYCTTGQIWAHSSYLGAFFNLTVADHLXVNI 258
QY 293 SNPSLLDPDQDATYFGAFKV 312
DB 259 SOLSLINFESKTFFGLYKL 278

RESULT 3

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-279 <TAK>
A;Cross-references: GB:U06948; NID:G473564; PIDN:AAA17800.1; PID:G473565
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
A;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A;Reference number: A53062; MUID:94185175; PMID:7511063
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-279 <TAK>
A;Cross-references: GB:U06948; NID:G473564; PIDN:AAA17800.1; PID:G473565

Query Match 10.9%; Score 182; DB 2; Length 279;
Best Local Similarity 22.7%; Pred. No. 1.2e-07;
Matches 72; Conservative 48; Mismatches 105; Indels 92; Gaps 13;

QY 13 RSSEEMSGGPGVHEGLHPAPSAPAPP-----PAASRSMFLALIGL 57
DB 38 RGPDRPPPPPPVPSPL-PPSPQPLPLPLKKNHNTNLWLVPPVPMVLVALVGMG 96
QY 58 LGQVVCVIALFLYRAQMDNRISEDTHCFYRILRLHENAGLDQSTLESEDITLPS 117
DB 97 LG-----MYQLFHLQKELAELEFTH-----LREFTNLSKVSFEKQIANPST-- 134
QY 118 MKQAFQAVOKELQHIIVGPORFSGAPAMGSMGLDVAQRKPEAQPPAHLTIN--AASIP 175
DB 135 -----PSE-----KPRSVAHLTGPNRSR 157
QY 176 SGSEKVTLSWYHGRGAKISNMTLSNGLRVNODGFFYLYANICFRHHETSGSVPTDY 235
DB 158 -----LEWEDTYGTALISGVKRYKGLVINEAGLYFYYSKYPR-GQSCNNQPLNH- 207
QY 236 QLVYVVKTSIKIPSSHNLMKGGSTKNWGNSEPHFYSINVGFFKLRAGEEISIOVSNP 295

DB 208 --KVYM--RNSKYPEDLVLM-EKRLNYCTTGQIWAHSSYLGAFFNLTSADHLXVNI 262
QY 296 SLILDPDQDATYFGAFKV 312
DB 263 SLINFESKTFFGLYKL 279

RESULT 4

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <RES>
A;Cross-references: EMBL:U11821; NID:G595430; PIDN:AAC50124.1; PID:G595431
R;Mit, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusanoto
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: GB:D38122; DBJ:D29820; NID:G601892; PIDN:BAA07320.1; PID:G1365
R;Schatzlein, C.E.
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X89102; NID:G887455; PID:G887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:G624627; PIDN:AAC50071.1; PID:G624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 173.5; DB 2; Length 281;
Best Local Similarity 21.2%; Pred. No. 6e-07;
Matches 67; Conservative 42; Mismatches 108; Indels 99; Gaps 9;

QY 22 PGVPHSGPLHPAPSAPAPPAPASR-----SMFLALIGL 58
DB 40 PGQRPPPPPPPPPPPPPPPPPPPPPLPLPLPLKKNHSTGLCLLVNFTMVLVALVGL 99
QY 59 GOVVCVIALFLYRAQMDNRISEDTHCFYRILRLHENAGLDQSTLESEDITLPS 118
DB 100 G-----MYQLFHLQ-----KELAELESTQHTA----- 124
QY 119 KQAFQAVOKELQHIIVGPORFSGAPAMGSMGLDVAQRKPEAQPPAHLTIN--AASIPS 176
DB 125 -----SSLEKQIGHSPPP-----KKELRKVAHLTGKNSRSM- 159
QY 177 GSHKVTLSWYHGRGAKISNMTLSNGLRVNODGFFYLYANICFRHHETSGSVPTDY 236
DB 160 -----LEWEDTYGTALISGVKRYKGLVINEAGLYFYYSKYPRGQSCNN-----LP 206

QY 237 LMVYVVKTSKIPSSHNLMKGGSTKNWSEHFFYSINVGFFKLRAGEEISIQVNSPS 296
 Db 207 LSHKVTMRNSKIPQDILVME-GROMSYCTGOMWARSYLIGAVFNLTSDHLVYVNSLS 265

QY 297 LLDPPDQDAYFGAFKV 312
 Db 266 LVNFESQTFEGYKYL 281

RESULT 5

I53476
 CD40 ligand - human
 N:Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
 C:Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
 R:Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
 MBO J. 11, 4313-4321, 1992
 A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
 A:Reference number: S28017; MUID:93049181; PMID:1385114
 A:Accession: S28017
 A:Molecule type: mRNA
 A:Residues: 1-261 <HOL>
 A:Cross-references: EMBL:Z15017; NID:938483; PIDN:CAA78737.1; PID:938484
 R:Spriggs, M.K.; Armitage, R.J.; Stockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
 J. Exp. Med. 176, 1543-1550, 1992
 A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin
 A:Reference number: JH0793; MUID:93094757; PMID:1281209
 A:Accession: JH0793
 A:Molecule type: mRNA
 A:Residues: 1-261 <SPR>
 A:Cross-references: GB:X67878; NID:938411; PIDN:CAA48077.1; PID:938412
 R:Experimental source: peripheral blood T-cell
 R:Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A.
 Eur. J. Immunol. 22, 3191-3194, 1992
 A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
 A:Reference number: S26694; MUID:93076854; PMID:1280226
 A:Accession: S26694
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-261 <GRA>
 A:Cross-references: EMBL:X68550; NID:937269; PIDN:CAA48554.1; PID:937270
 R:Gauchat, J.F.; Aubry, J.P.; Marzel, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
 FEBS Lett. 315, 259-266, 1993
 A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
 A:Reference number: S28852; MUID:93138085; PMID:7678552
 A:Accession: S28852
 A:Molecule type: mRNA
 A:Residues: 1-261 <GAN>
 A:Cross-references: EMBL:L07414; NID:9180123; PIDN:AAA35662.1; PID:9180124
 A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
 C:Genetics:
 A:Gene: GDB:CD40LG; HIGM1; IMD3
 A:Cross-references: GDB:120632; OMIM:308230
 A:Map position: Xq26-Xq26
 C:Keywords: glycoprotein; transmembrane protein
 F:13-44/Domain: transmembrane #status predicted <PMM>
 F:45-261/Domain: extracellular #status predicted <EXT>
 F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.28; Score 171.5; DB 2; Length 261;
 Best Local Similarity 25.28; Pred. No. 8e-07;
 Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;

QY 33 APSAPAPAPPAAASRMFLALLGLIGGVVCSIALF-LYFRAQMDPNRISEDSHCFYRI 91
 Db 9 SPRAATGLP--ISKIFWLLTVFLITQMGSAFVFLHRLD--KIEDER----- 57

QY 92 LRLHE-----NAGLDSTLESDTLPSDCRMKQAFQAGVQKELQHVGPORFS 140
 Db 58 -NLHEDFVFNKTIQRCTNGERSLSL-----NCEIKSQFEGV-KDIM-----LN 101

QY 141 GAPAMGSLWDAORKEPAQPFALHTINAASIPSGSHKVTLSWYHGRWAKISN--M 198
 Db 102 KEETKENSF--EMKGDONPQIAAHV-----ISASSTKTSVLQWAEKGYTMMNLV 153
 QY 199 TISNGK-LRVNODGFYLYANTCF-RHHTSGSVPTDYQLQVMVYVVKTSIKIPSSHN--L 254
 Db 154 TLENGKQLTVKROGLYIIYAQVTFCSNREASSQAP-----FIASLCLKSPGFERIL 205
 QY 255 MKGGSTKNWSEHFFYSINVGFFKLRAGEEISIQVNSPSLLDPDQDAYFGAFKV 312
 Db 206 LRAANTH--SSAKPCQQQSHLGGVFELOPGASVFVNVDPSQVSHGTGFTSGLLKL 261

RESULT 6

S21738
 CD40 ligand - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
 C:Accession: S21738
 R:Armitage, R.J.; Fanslow, W.C.; Stockbine, L.; Sato, T.A.; Clifford, K.N.; Macdu
 ; Cosman, D.; Spriggs, M.K.
 Nature 357, 80-82, 1992
 A:Title: Molecular and biological characterization of a murine ligand for CD40.
 A:Reference number: S21738; MUID:92244364; PMID:1374165
 A:Accession: S21738
 A:Molecule type: mRNA
 A:Residues: 1-260 <ARM>
 A:Cross-references: EMBL:X65453; NID:950351; PIDN:CAA46448.1; PID:950352
 C:Keywords: glycoprotein; transmembrane protein
 F:23-46/Domain: transmembrane #status predicted <PMM>
 F:47-260/Domain: extracellular #status predicted <EXT>
 F:239/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.48; Score 157; DB 2; Length 260;
 Best Local Similarity 24.88; Pred. No. 1.3e-05;
 Matches 75; Conservative 51; Mismatches 105; Indels 72; Gaps 16;

QY 32 PAPSAPAPAPPAAASRMFLALLGLI-GOVVCSIALFLYFRAQMDPNRISEDSHCFYR 90
 Db 8 PPSRVATGLP--ASMKIFWLLTVFLITQMGSAFVFLHRLD--KVEE----- 56

QY 91 LRLHE-----NAGLDSTLESDTLPSDCRMKQAFQAGVQ-----KELQHV 134
 Db 57 -VNLHEDFVFIKLRCKNKGESLSL-----NCEMRQFEDLVKDTLNKE----- 103

QY 135 GPORFGAPAMGSLWDAORKEPAQPFALHTINAASIPSGSHKVTLSWYHGRWAK 194
 Db 104 -----EKKENSF--EMQGEDPQIAAHVYVSEA-----NSNAASVLQWAKKGYTM 147

QY 195 ISNMT-LSNGK-LRVNODGFYLYANTCF-RHHTSGSVPTDYQLQVMVYVVKTSIK--IP 249
 Db 148 KSNLVMLENGKQLTVRREGLYIYVTVTFCSNREPSQRP-----FIVGLWLFPSIG 199

QY 250 SSNLRKGGSTKNWSEHFFYSINVGFFKLRAGEEISIQVNSPSLLDPDQDAYFGA 309
 Db 200 SERILLKAANTHSSQLCEQQ--SVHLGGVFELOPGASVFVNVTASQVTHRVGFSFGL 257

QY 310 FKV 312
 Db 258 LKL 260

RESULT 7

JQ1344
 tumor necrosis factor alpha precursor - horse
 N:Alternate names: cachectin; TNF alpha
 C:Species: Equus caballus (domestic horse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: JQ1344
 R:Su, X.; Morris, D.D.; McGraw, R.A.
 Gene 107, 319-321, 1991
 A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necr
 A:Reference number: JQ1344; MUID:92084125; PMID:1748301

A;Molecule type: mRNA
A;Residues: 1-235 <PEN>
A;Cross-references: GB:M17131; NID:g202084; PIDN:AAA0458.1; PID:g202085
R;Transen, L.; Muller, R.; Marmencout, A.; Tavernier, J.; van der Heyden, J.; Kawashiri
Nucleic Acids Res 13, 4417-4429, 1985
A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic e
A;Reference number: A23127; MUID:85242112; PMID:2989794
A;Accession: A23127
A;Molecule type: mRNA
A;Residues: 1-235 <FRA>
A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845
R;Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resu
A;Reference number: A34251; MUID:89380231; PMID:277790
A;Accession: A34251
A;Molecule type: protein
A;Residues: 70-87 <CSE>
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated reg
A;Reference number: I59058; MUID:86149365; PMID:2419912
A;Accession: I59058
A;Status: preliminary; translated from GB/EMBL/DDBB
A;Molecule type: mRNA
A;Residues: 1-230, R', 232-235 <RES>
A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA0457.1; PID:g202083
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylated forms of murine tum
A;Reference number: A36696; MUID:91097531; PMID:2268312
A;Accession: A36696
A;Molecule type: protein
A;Residues: 80-85, X', 87-99 <SHE>
C;Genetics:
A;Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage;
F;80-235/Product: tumor necrosis factor #status experimental <MA>
F;20/Binding site: myristate (lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

Query Match 8.7%; Score 146.5; DB 1; Length 235;
Best Local Similarity 25.6%; Pred. No. 8.5e-05;
Matches 51; Conservative 36; Mismatches 67; Indels 45; Gaps 11;

QY 133 IVGPORP-----SGAP-----AMEGSLDVAQRGKPEAOPFAHLTINAASIPSGSHKVTLIS- 184
 :||||| :||||| :||||| :|||||
Db 55 VIGPQRDEKPNGLPLISSNAQTLLRSSQNSSD-KPAHVAVAN-----HQVEEQL 105

QY 185 SWHEDRCWAKISN-WTILSNGLRLVNDGFYYLIYANICPRHHETSGSVPTDIQLMYVVK 243
 || :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
Db 106 EWLSQRSARALLANGMDLKDNLQVVPADGLYLIVYSQVLFK-----GGCCPDYV-LTHTVS 159

QY 244 -----TSIKPSHNLMKGSTKNWGSNFHFYSINVGFFFLKAGEETS! 290
 :::||: :::||: :::||: :::||: :::||:
Db 160 RFALSYOEKYNNLSAVKSPCKDPPEGAELKPW-----YEPIYLGVFQLEKGDQLSA 212

QY 291 QVSNPSLLD-PDQATYFG 308
 :|| :|| :||
Db 213 EVNLPKYLDFAESGVYFG 231

RESULT 9
S22052
tumor necrosis factor alpha precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S22052
R;Santanwala, M.; Edwards, A.

C;Superfamily: tumor necrosis factor

RESULT 12

OWHUN
tumor necrosis factor alpha precursor [validated] - human
N:Alternate names: cachectin; TNFA
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R:Medwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
Nucleic Acids Res. 13, 6361-6373, 1985
A:Title: Human lymphotxin and tumor necrosis factor genes: structure, homology and chro
A:Reference number: A93585; MUID:86016093; PMID:2995927
A:Accession: A93585
A:Molecule type: DNA
A:Residues: 1-233 <NED>
A:Cross-references: GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
R:Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A:Reference number: S36152; MUID:93272029; PMID:8499947
A:Accession: S36153
A:Status: nucleic acid sequence not shown; translation not shown
Molecule type: DNA
Residues: 1-233 <IRI>
A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A:Title: Human tumour necrosis factor: precursor structure, expression and homology to l
A:Reference number: A93351; MUID:85086244; PMID:6392892
A:Accession: A93351
A:Molecule type: mRNA
A:Residues: 1-233 <PEN>
A:Cross-references: GB:X02910; NID:g37209; PIDN:CAA26669.1; PID:g37210
A:Note: this protein was isolated from the monocytic-like cell line HL-60 from a promyeloc
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.;
Science 228, 149-154, 1985
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A:Reference number: A44189; MUID:85142190; PMID:3856324
A:Accession: A44189
A:Molecule type: mRNA
A:Residues: 1-62, 5', 64-233 <WAN>
A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
Lymphokine Res. 7, 175-185, 1988
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A:Reference number: A61478; MUID:86301617; PMID:2841543
A:Accession: B61478
A:Molecule type: protein
A:Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
R:Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
J. J. Biochem. 152, 515-522, 1985
A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A:Reference number: I53311; MUID:86030296; PMID:3932069
A:Accession: I53311
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-233 <MAX>
A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
A:Experimental source: U-937 cells
R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A:Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A:Reference number: S62610; MUID:96202967; PMID:8631363
A:Accession: S62610
A:Molecule type: protein
A:Residues: 77-99 <TAK>
R:D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter regio
A:Reference number: I54522; MUID:94102809; PMID:7903959
A:Accession: I54522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-8 <DAL>
A:Cross-references: GB:S68530; NID:g544751
R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific
A:Reference number: A59163; MUID:93018820; PMID:1402651
A:Contents: annotation; identification of myristylated lysines
R:Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Morfat, B.; Spencer, S.A.; Henzel, W.J.; J.
J. Biol. Chem. 260, 2345-2354, 1985
A:Title: Human tumor necrosis factor. Production, purification, and characterization
A:Reference number: A92511; MUID:85130974; PMID:3871770
A:Contents: annotation; disulfide bond
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after indu
out detriment to normal cells. It can also act synergistically with interferon gamma
C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes cl
ut are produced by different cell types and have different induction kinetics.
C:Genetics:
A:Gene: GDB:TNF; TNFA
A:Cross-references: GDB:120441; OMIM:191160
A:Map position: 6p21.3-6p21.3
A:Introns: 62/3; 78/1; 94/1
C:Complex: homotrimer
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine;
F:1-76/Domain: propeptide #status predicted <PRO>
F:77-233/Product: tumor necrosis factor #status experimental <MAT>
F:19/20/Binding site: myristate (Lys) (covalent) #status experimental
F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F:145-177/Disulfide bonds: #status experimental
Query Match 8.3%; Score 139.5; DB 1; Length 233;
Best Local Similarity 24.9%; Pred. No. 0.00032;
Matches 48; Conservative 34; Mismatches 76; Indels 35; Gaps 9;
QY 133 IVGPOREFGAPAMGSGWLDVAORG---PEAQPFAHLINAASIPSGSHKVTLSWYHD 189
DB 55 VIGPOREFPRDLISLISPLAQAVRSRRTPSPKPVAVHVN----PQAGQL---OWLNR 107
QY 190 RGWAKISN-MTLNGLKRLRYNODGYLYYANICFRHETSGSVPTDYQL-----WY 240
DB 108 RANALLANGVELRDNLVVPSEGLYLYSQVLFK----GOGCPSTHVLTHFTISIAVS 163
QY 241 VVK-----TSIKIPSSHNLMKGSTKNWNSSEHFYSINVGGFKLRAGEEISIQVNSP 296
DB 164 QTKVLLLSAISKPCQRETPGEAKPW-----YEPIYLGVPQLEKGRLSAEINRPD 216
QY 297 LLD-PDQDATYFG 308
DB 217 YLDFAESGGVYFG 229
RESULT 13
A25451
tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: A25454; A25451; JS0727
R:Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayash
DNA 5, 149-156, 1986
A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding fo
A:Reference number: A25454; MUID:86219711; PMID:3519137
A:Accession: A25454
A:Molecule type: mRNA
A:Residues: 1-234 <ITO>
A:Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R:Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace,
DNA 5, 157-165, 1986
A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A:Reference number: A25451; MUID:86219712; PMID:3519138
A:Accession: A25451
A:Molecule type: DNA
A:Residues: 1-234 <ITO>

A>Note: this sequence differs from that shown in having a Gln inserted between residues R;Shahov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990

A>Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF- α , TNF- β , and TNF- γ .
A:Reference number: JH0309; MUID:91065534; PMID:2249779

A:Accession: J50727

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-62, Q' 63-234 <SHA>

A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756

C:Genetics:

A:Introns: 62/3; 80/1; 96/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane

F:1-81/Domain: propeptide status predicted <PRO>

F:82-234/Product: tumor necrosis factor status predicted <MAT>

F:19,20/Binding site: myristate (Lys) (covalent) status predicted

F:83/Binding site: carbohydrate (Ser) (covalent) status predicted

F:147-178/Disulfide bonds: status predicted

Query Match 8.28; Score 137.5; DB 1; Length 234;

Best Local Similarity 22.68; Pred. No. 0.00048;

Matches 68; Conservative 31; Mismatches 99; Indels 103; Gaps 12;

Qy 27 EGPLHPAPAPAPAPPAASR-----SMELALIGLIGVVCSTALFLYFRAQMDPNKRIS' 81

Db 14 EGPL-----PKAGGQGGKRCCLSLFSLVAGATTFC-----LLHFRVIGPQEEES 63

Qy 82 EDSTHCFYRILRLHENAGLDSTLESDTLPSDCRRMKQAFQGAQVOKELQHVIGPQRFSG 141

Db 64 PNNLHLV-----NPVQAVMTLRS-----ASRALSDRPLAHVV----- 95

Qy 142 APAMGSLDVAORGPAPAPPAFAHILNNAASIPSGSHKVTLSWYHGRGWAKISN-MTL 200

Db 96 ANPQVEGQ-----LQWLSQRANALLANGMKL 121

Qy 201 SNGKLNVODGFYLYANICPRHETSGVPTDYLQLMVYVTKSIRKIPSSHNLKMG--- 257

Db 122 TDNLVVPADGLLYISQVLF-----SGQGRSVLLTHVSRFVAVSPKVNLLSAIKS 176

Qy 258 -----GSTRKWSGNSEPHFYSINVGFFKLAGEEISIQVSNPSSLDPDQDATYF 307

Db 177 PCHRETPEAPMAW-----YEPYILGGVGFQLEKGRDLSTEVNQPEYLDLAESGGQVYF 229

Qy 308 G 308

Db 230 G 230

RESULT 14

I54490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000

A:Accession: I54490

R:Crew, M.D.; Filipovsky, M.E.

Immunogenetics 35, 351-353, 1992

A>Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus

A:Reference number: I54490; MUID:92218012; PMID:1348497

A:Accession: I54490

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 <RES>

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:

A:Gene: pTNF

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation

F:19,20/Binding site: myristate (Lys) (covalent) status predicted

F:84/Binding site: carbohydrate (Ser) (covalent) status predicted

Query Match

8.18; Score 135.5; DB 2; Length 235;

Best Local Similarity 25.18; Pred. No. 0.0007;

Matches 51; Conservative 31; Mismatches 68; Indels 53; Gaps 10;

Qy 133 IVGPQRSGAP-----AMMEGSLDVAORGPAPPAFAHILNNAASIPSGSHKVTLSWY 185

Db 55 VIGPQREKFPNNLPIIGSMAQTILTRSSSQSSD-KPVAHVAN-----HOVDSQL 105

Qy 186 WYHGRGWAKISNMTLSNG-KLRVNO-----DCGYLYLVANICFRHETSGSVPTDYLQLMV 239

Db 106 EWLRSRG-----ANALLANGMDLKDNLVLPADGLLYISQVLFKGGCCSYV-----LLT 155

Qy 240 YVVK-----TSIKIPSSHNLKGGSTKNSGNSEPHFYSINVGFFKLAGEEISIQ 286

Db 156 HTVSRFAVSIEDKVNLLSAIKSPCKETPEGSELKPM-----YEPYILGGVGFQLEKGRD 208

Qy 287 EISQVSNPSSLDPDQDATYF 308

Db 209 RLAEVNLPRYLDFAESGQVYF 231

RESULT 15

I24642

tumor necrosis factor alpha precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

A:Accession: I46047; S24642

R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A>Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin

A:Reference number: I46046; MUID:94083525; PMID:8260599

A:Accession: I46047

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-233 <CL2>

A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C:Genetics:

A:Gene: TNFA

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:20/Binding site: myristate (Lys) (covalent) status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) status predicted

F:145-177/Disulfide bonds: status predicted

Query Match 8.08; Score 133.5; DB 1; Length 233;

Best Local Similarity 25.88; Pred. No. 0.001;

Matches 51; Conservative 30; Mismatches 72; Indels 45; Gaps 11;

Qy 133 IVGPQR--FSGAPAMMEGSLDVAORGPAPPAFAHILNNAASIPSGSHKVTLSWY 187

Db 55 VIGPQREKFPNNLPIIGSMAQTILTRSSSQSSD-KPVAHVAN-----INSFG 100

Qy 188 HDRGWAKISNMTLSNG-KLRVNO-----DCGYLYLVANICFRHETSGSVPTDYLQLMV 231

Db 101 QLRWDSYANALMANGVKLEDNQLVVPADGLLYISQVLFKGGCCSYV-----INSFG 160

Qy 232 TDYLQLMVYVTKSIRKIPSSHNLKGGSTKNSGNSEPHFYSINVGFFKLAGEEISIQ 291

Db 161 VSY-QTRVNL-SAIKSPCHRETPEWAEAKPW-----YEPYILGGVGFQLEKGRDLSAE 211

Qy 292 VSNPSSLDPDQDATYF 308

Db 212 INLPDYLAESGQVYF 229

Search completed: April 16, 2003, 12:20:42

Job time : 17.5 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:16:16 ; Search time 9.5 seconds
(without alignments)
1379.634 Million cell updates/sec

Title: US-09-787-126-4

Perfect score: 1675

Sequence: 1 MRRASRDYKYLRSSEMGs.....LLDPDQDARYFGAKVQDID 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	316	1	TN11_MOUSE
2	1597	95.3	318	1	TN11_MOUSE
3	1417.5	84.6	317	1	TN11_HUMAN
4	258.5	15.4	281	1	TN10_HUMAN
5	244	14.6	291	1	TN10_MOUSE
6	188.5	11.3	261	1	TN10_MOUSE
7	185.5	11.1	261	1	TN10_MOUSE
8	183	10.9	278	1	TN10_MOUSE
9	182.5	10.9	261	1	TN10_MOUSE
10	182	10.9	279	1	TN10_MOUSE
11	179.5	10.7	282	1	TN10_MOUSE
12	178	10.6	280	1	TN10_MOUSE
13	177	10.6	280	1	TN10_MOUSE
14	176.5	10.5	261	1	TN10_MOUSE
15	173.5	10.4	281	1	TN10_MOUSE
16	171.5	10.2	261	1	TN10_MOUSE
17	168.5	10.1	272	1	TN10_MOUSE
18	164	9.8	260	1	TN10_MOUSE
19	159.5	9.5	261	1	TN10_MOUSE
20	157	9.4	234	1	TN10_MOUSE
21	157	9.4	260	1	TN10_MOUSE
22	154	9.2	260	1	TN10_MOUSE
23	151	9.0	240	1	TN10_MOUSE
24	149	8.9	234	1	TN10_MOUSE
25	148.5	8.9	233	1	TN10_MOUSE
26	147.5	8.8	233	1	TN10_MOUSE
27	147.5	8.8	310	1	TN10_MOUSE
28	146.5	8.7	235	1	TN10_MOUSE
29	146.5	8.7	239	1	TN10_MOUSE
30	145	8.7	260	1	TN10_MOUSE
31	143.5	8.6	233	1	TN10_MOUSE
32	143.5	8.6	233	1	TN10_MOUSE
33	141	8.4	234	1	TN10_MOUSE

34	140	8.4	174	1	TN15_HUMAN
35	140	8.4	233	1	TNFA_FELCA
36	139.5	8.3	233	1	TNFA_CANFA
37	139.5	8.3	233	1	TNFA_HUMAN
38	139	8.3	234	1	TNFA_CAPHI
39	137	8.2	235	1	TNFA_RABIT
40	135.5	8.1	235	1	TNFA_PERLE
41	134.5	8.0	240	1	TN14_HUMAN
42	133.5	8.0	233	1	TNFA_BOVIN
43	133	7.9	232	1	TNFA_PIG
44	129.5	7.7	233	1	TNFA_MARMO
45	129.5	7.7	235	1	TNFA_RAT

ALIGNMENTS

RESULT 1

ID	TN11_MOUSE	1 STANDARD;	PRT;	316 AA.
AC	Q35235; Q35306; Q9R1V0; Q9JJK8; Q9JJK9;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor) (OCIF).			
GN	TNFRSF11 OR RANKL OR TRANCE OR OPGL.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Hybridoma;			
RX	MEDLINE=37460112; PubMed=9312132;			
RA	Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.;			
RT	"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";			
RL	J. Biol. Chem. 272:25190-25194(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Thymic lymphoma;			
RX	MEDLINE=98032977; PubMed=9367155;			
RA	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D., Galibert L.;			
RT	"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";			
RL	Nature 390:175-179(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=98227661; PubMed=9568710;			
RA	Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.;			
RT	"Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation.";			
RL	Cell 93:165-176(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Bone marrow stroma;			
RX	MEDLINE=9818248; PubMed=9520411;			
RA	Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M., Mochizuki S.-I., Tomoyasu A., Yan K., Goto M., Murakami A., Tsuda E., Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;			

DR	EMBL:	AF013171;	AAC51762.1;	-
DR	EMBL:	AB037599;	BAA90488.1;	-
DR	HSSP:	P50591;	IDOG.	
DR	Genew:	HGNC:	I1926;	TNFSF11.
DR	MTM:	602642;	-	
DR	InterPro:	IPR003636;	TNF_abc.	
DR	InterPro:	IPR000478;	TNF_family.	
DR	Pfam:	PF00229;	TNF; 1.	
DR	PfDom:	PD002012;	TNF_abc; 1.	
DR	SMART:	SM00207;	TNF; 1.	
DR	PROSITE:	PS00251;	TNF_1;	FALSE_NEG.
DR	PROSITE:	PS00049;	TNF_2;	1.
KW	Cytokine:	Differentiation;	Receptor;	Glycoprotein; Transmembrane;
KW	Signal-anchor:	Alternative splicing.		
FT	FT	CHAIN	1	317
FT	FT	CHAIN	140	317
FT	FT	DOMAIN	1	47
FT	FT	TRANSMEM	48	68
FT	FT	DOMAIN	69	317
FT	FT	SITE	139	140
FT	FT	CARBOHYD	171	171
FT	FT	CARBOHYD	198	198
FT	FT	VARSPLIC	1	47
FT	FT	VARSPIC	1	73
FT	FT	CONFLICT	194	194
FT	FT	SEQUENCE	317 AA;	35478 MW; 766176446348097F CRC64;
QY	Query Match		84.6%;	Score 1417.5; DB 1; Length 317;
Db	Best Local Similarity		84.3%;	Pred. No. 5e-110;
	Matches 268;	Conservative 16;	Mismatches 31;	Indels 3; Gaps
QY	1	MRRASRDYGYILRSSEMGGCPVPREGPLHPAPSAPAPPAPPAASRMFLALLGLGLGQ	60	
Db	1	MRRASRDYTYLRLSEMGEGGPARGEPGLH-APPDPAPHQPAPPAASRMFMVALLGLGLGQ	59	
QY	61	VVCISALFLYFRAQMDPNRIESTSTHCIFRLRLHENAGLDSTLESDT--LPDSCRM	118	
Db	60	VVCISVALFFYFRAQMDPNRISEDCTHCITRYLLRLHENADFDTLESQDTKLIPDSCRRI	119	
QY	119	KQAFOGAVOKELHIYQPGRFSGAPAMEGSWLDVAQRGKPEAQPPAHLTINAAISIPGS	178	
Db	120	KQAFOGAVOKELHIYQSQHIRAEKAMVDGSLDLAKRSKLEAQPPAHLTINATDIPGS	179	
QY	179	HKVTLSWSYHDRCGWAKISNTLTNSGLRVNDGFYYLIYANICFRHHETSGSVPTDYQLQM	238	
Db	180	HKVLSLSWSYHDRCGWAKISNTLTNSGLRVNDGFYYLIYANICFRHHETSGDLATEYQLQM	239	
QY	239	VYVKTSIKIPLSSHNLMKGSTKNWGSNEFHYSINVGGFKLAGREISIQVSNPSLL	298	
Db	240	VYVKTSIKIPLSSHTLMKGSYKNWGSNEFHYSINVGGFKLAGREISIEVSNPSSL	299	
QY	299	DDPDQATYFGAFKVQDID 316		
Db	300	DDPDQATYFGAFKVQDID 317		
RESULT 4				
TN10_HUMAN		STANDARD;	PRT;	281 AA.
AC	TN10_HUMAN			
ID	P50591;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related			
DE	apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).			
GN	TNFSF10 OR TRAIL OR APO2L			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			

RN RP SEQUENCE FROM N.A.
 RX MEDLINE-96111955; PubMed-8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF
 RL family that induces apoptosis.";
 RL Immunity 3:673-682(1995).
 [2]
 RN RP SEQUENCE FROM N.A.
 RX TISSUE-Placenta;
 RC MEDLINE-96278649; PubMed-8663110;
 RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
 RA Askenazi A.;
 RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
 RL necrosis factor cytokine family.";
 RL J. Biol. Chem. 271:12687-12690(1996).
 [3]
 RN RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 RX MEDLINE-20017054; PubMed-10543288;
 RA Hynowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
 RA Kelley R.F., Askenazi A., de Vos A.M.;
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 RL complex with death receptor 5.";
 RL Mol. Cell 4:563-571(1999).
 [4]
 RN RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RX PubMed-10542098;
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Screaton G.R.;
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RL specificity in apoptotic initiation.";
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 [5]
 RN RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RX MEDLINE-994113670; PubMed-10485660;
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 RA Sung Y.C., Oh B.-H.;
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
 RL selective antitumor activity.";
 RL Immunity 11:253-261(1999).
 -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 -1- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 CC trimer.
 -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
 CC AND PROSTATE.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 DR EMBL; U37518; AAC50332.1; -
 DR EMBL; U57059; AAB01233.1; -
 DR Genbank; HGNC:11925; TNFSF10.
 DR MIM; 603598; -
 DR PDB; 1D0G; 22-OCT-99.
 DR PDB; 1D4V; 01-NOV-99.
 DR PDB; 1D2Q; 11-FEB-00.
 DR InterPro; IPR003636; TNF abc.
 DR InterPro; IPR000478; TNF_family.

DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 KW Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
 FT Zinc; 3D-structure.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 39 281 (POTENTIAL).
 FT METAL 230 230 EXTRACELLULAR (POTENTIAL).
 SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAB2F6D CRC64;
 ZINC.
 Query Match 15.48; Score 258.5; DB.1; Length 281;
 Best Local Similarity 26.48; Pred. No. 3e-14; Indels 51; Gaps 10;
 Matches 78; Conservative 54; Mismatches 113;
 QY 43 PAASRSMFLALLGLGQVGVCSIALFLYFRAQMD--PNRISEDSHCFYRILRLHENAGL 100
 DB 10 PSLGTCVLIIVFVLQSLCVAVTYVFTNELKQMDKYSGIACF-----LKEDDSY 64
 QY 101 QDSTLESDTLDPDCRRMKQAFQGVAK-----ELQHVGPQRFSGAPAM 146
 DB 65 WDP--NDESMNSPCWQVQWLRQLVRKMLRTSEETISTVQEKQNISPL----- 113
 QY 147 EGSWLDVAQRGPEAQPEAHLT-----INAAISIPSGSHKVTL-----SSWYHDR-GWAKIS 196
 DB 114 -----VREGRQPRVA--AHITGTGRSNTLSSPSKNEKALGRKINSWESSRSGHSFLS 165
 QY 197 NMTLSNGKLRVNDGFIYLYANICFRHETSGVPTDYLQLMVYVYKTSIKIPSSHNLMK 256
 DB 166 NLHLANGELVHERGFYIYSOTYFRQEEIKENTKNDKQWQYIYKYT-SYDPDILLMK 224
 QY 257 GGSTKNWSGNSGFHYFSINVGGFKLRAEEISIOVSNPSLLDPDODATYFGAFKY 312
 DB 225 SARNCSKSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280
 RESULT 5
 TN10_MOUSE
 ID TN10_MOUSE STANDARD; PRT: 291 AA.
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96111955; PubMed-8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF
 RL family that induces apoptosis.";
 RL Immunity 3:673-682(1995).
 -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR EMBL: 037522; AAC52345.1;
 DR HSP: P50591; 1D0G.
 DR MGD: MGI:107414; Tnfsl10.
 DR InterPro: IPR003636; TNE_abc.
 DR Pfam: PF00229; TNE; 1.
 DR ProDom: PD002012; TNE; 1.
 DR SMART: SM00207; TNE; 1.
 DR PROSITE: PS00251; TNE_1; 1.
 DR PROSITE: PS50049; TNE_2; 1.
 KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT TRANSMEM 39 291 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
 ST SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 14.6%; Score 244; DB 1; Length 291;
 Best Local Similarity 27.5%; Pred. No. 4.9e-13;
 Matches 83; Conservative 50; Mismatches 111; Indels 58; Gaps 15;

QY 52 ALLIGLIGLQ-----VVCSTAL-----FLYRAQMD--PNRISESTHCFYRL 92
 DB 6 ALKDLFSQHFRAWVICVILLVQLQAVSVAVTYFTNEMKQLQDNYSKIGLACFSK-- 63
 QY 93 RLHENAGLQDSTLESDTLPDSC-----RRMKAQAFQAVOKELQHVIG--PQFSGAPAMM 146
 DB 64 ---TDEFDWST--DGEILNRCPLQVKRQLYQIEVTLRTFDITVPEKQLSTPPPLP 118
 QY 147 EGSWLDVAORGPEAPQFAHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS 196
 DB 119 RG-----GRPQ-KVAAHITGTRNSALIPISKDKGTGLQKIESSESRKGHSFLN 169
 QY 197 NMTLSNGKLVNQDGYLYANICFRHHE---TSGSVPTDYL---QIMYVYVKTISKIPS 250
 DB 170 HVLFRNGELVIEQGLYIYSQTYFRFOEADAKRVSKDKVTKQLQVQIYKYIT-SYDP 228
 QY 251 SHNLMGGSTKNWGNSEHFYSINVGPFKLRAGEISIOVSNPILDDPDQDQATYFGAF 310
 DB 229 PIVLMSARNSCWSRDREGLYSIYOGGLFELAKNDRIFFSVTNEHMLDLDQASFFGAF 288
 311 KV 312
 DB 289 LI 290

RESULT 6
 TNF5_CALJA STANDARD; PRT; 261 AA.
 ID TNF5_CALJA
 AC Q9BDN3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
 DE L) (CD154 protein).
 GN TNFSF5 OR CD401G OR CD40L.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 OC Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;

RX MEDLINE-21383618; PubMed-11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 FT "Cloning, sequencing, and homology analysis of nonhuman primate
 FT Fas/Fas-ligand and co-stimulatory molecules";
 RL Immunogenetics 53:315-328(2001).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
 CC proliferation in the absence of co-stimulus as well as TGE
 CC class switching (By similarity).
 CC -!- SUBUNIT: HOMOTRIMER (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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DR EMBL: AF344844; AAK37603.1;
 DR HSP: P29965; ITALY.
 DR InterPro: IPR003263; TNE 5.
 DR InterPro: IPR003636; TNE_abc.
 DR InterPro: IPR000478; TNE_family.
 DR Pfam: PF00229; TNE; 1.
 DR ProDom: PD002012; TNE_abc; 1.
 DR ProDom: PD008600; TNE 5; 1.
 DR SMART: SM00207; TNE; 1.
 DR PROSITE: PS00251; TNE_1; 1.
 DR PROSITE: PS50049; TNE_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 261 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT CHAIN 113 261 MEMBER 5, MEMBRANE FORM.
 FT DOMAIN 1 22 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT TRANSMEM 23 43 MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
 FT DOMAIN 44 261 CYTOPLASMIC (POTENTIAL).
 FT SITE 112 113 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 178 218 CLEAVAGE (BY SIMILARITY).
 FT CARBOHYD 240 240 N-LINKED (GLCNAC...) (POTENTIAL).
 ST SEQUENCE 261 AA; 29360 MW; 10CA58BD923734EB CRC64;

Query Match 11.3%; Score 188.5; DB 1; Length 261;
 Best Local Similarity 25.8%; Pred. No. 1.7e-08;
 Matches 77; Conservative 49; Mismatches 110; Indels 63; Gaps 16;

QY 32 PAPSAPAPAPPAAASRMFLALIGLIGLQGVVCSIALF-LYFRAQMDPNRISESTHCFYR 90
 DB 8 PVPRSAATGPP--VSMKIFMYLLTVFLITQMGSLGSAFVYLHRRLD--KIEDER----- 57
 QY 91 ILRLHE-----NAGLQDSTLESDTLPDSCRRMKAQAFQAVOKELQHVIGPQRF 139
 DB 58 ---NLHEDFVFMKTQRCNTGERSLSLL-----NCEEIKSQEGFV-KDIM-----L 100
 QY 140 SGAPAMGSEWLDVAORGPEAPQFAHLTINAAIPSGSHKVTLSWYHDRGWAKISN-- 197
 DB 101 NKEEKKNSF--EMQKQDNQPIAAHV-----ISEASKTTSVLQWAEKGYTMSNNL 152
 QY 198 MTLNCK-LRVNQDGYLYANICF-RHHTSGSVPTDYLQLMVYVYVYKSIKIPSHN-- 253
 DB 153 VTLNGKQLTVKRGQGLYIYQVTFCSNREASSQAP-----FIASLCLKPPNRFERI 204
 QY 254 LMKGSTKNWGNSEHFYSINVGPFKLRAGEISIOVSNPILDDPDQDQATYFGAFV 312
 DB 205 LLRAANTH--SSAKPGQGSIHLLGGIFELQPGASVFNVTDFPSQVSGHGFTSFGLKL 261

-1- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).

-1- SUBUNIT: HOMOTRIMER (By similarity).

-1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

-1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; AF344860; AKK37542.1; HSP; P29965; ITALY. InterPro: IPR003263; TNF_5. InterPro: IPR003636; TNF_ab. InterPro: IPR000478; TNF_family. Pfam; PF00229; TNF; 1. ProDom; PD002012; TNF_ab; 1. ProDom; PD008600; TNF_5; 1. SMART; SM00207; TNF; 1. PROSITE; PS00251; TNF_1; 1. PROSITE; PS00049; TNF_2; 1. Cytokine; Transmembrane; Glycoprotein; Signal-anchor. TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, MEMBRANE FORM. TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, SOLUBLE FORM (BY SIMILARITY). CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL). EXTRACELLULAR (POTENTIAL). CLEAVAGE (BY SIMILARITY). POTENTIAL. N-LINKED (GLCNAC...) (POTENTIAL).

Query Match 10.9%; Score 182.5; DB 1; Length 261; Best Local Similarity 25.8%; Pred. No. 5.2e-08; Matches 77; Conservative 49; Mismatches 110; Indels 63; Gaps 16;

	CHAIN	113	261	
DR	CHAIN	113	261	
DR	DOMAIN	1	22	
DR	TRANSMEM	23	43	
DR	DOMAIN	44	261	
DR	SITE	112	113	
DR	DISULFID	178	218	
DR	CARBOHYD	240	240	
DR	SEQUENCE	261 AA;	29357 MW;	85E1388B507901B5 CRC64;
Qy	32	PAPSAPAPPPASRSFMFLALLGLGQVVCSTIALF-LYFRAQMDPNRISESTHCYR	90	
Db	8	PAPSAATGLP--VSMKIFMTYLLVFLITOMIGSALFAVYLHRRID--KIEDR-----	57	
Qy	91	ILRLHE-----NAGLDSTLESDYLPDCRRMKQAFQAVOKELHIVGPORF	139	
Db	58	--NLHEDVFVMTQRCMTGERSLSL-----NCEIKSQFGFV-KDLM-----	100	
Qy	140	SGAPAMMGSLVDVAQRKPAQPAHLTINAAISPGSHKVTLSWYHWRGAKISN--	197	
Db	101	NKEKKENSF--EMKGDQNPQAAHV-----ISEASSTVSLVQAEKGYTMSNNL	152	
Qy	198	MTLSNGK-LRYNDGFFYLYANICF-RHETSGSVPTDYLOLWVYVVKTSIKIPSSH--	253	
Db	153	VTLENGKQLTVKRGLYIYIAQVTFCSNREASSQAP-----FIASCLKPPNRPRI	204	
Qy	254	LMKGSYKNSGNSEFHEYSINVGFFFKLAGEELISIOVNSPLDPPQDATYPAKV	312	
Db	205	LLRAANTH--SSAKPCGOOSTHLGSGIFELQPGASVFNVTDPQSVSGTGTFSGLLKL	261	

RESULT 10
TNF6_MOUSE STANDARD; PRT; 279 AA.
ID TNF6_MOUSE
AC P41047; Q9R1F2;

[illegible]

SEQUENCE FROM N.A.
Wilkinson J.;
Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[7]
SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Blood;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
[8]
SEQUENCE OF 1-10 FROM N.A.
TISSUE=Blood;
Matsumura M., Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
[9]
CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
Terskikh A., Peitsch M.C., Tschopp J.;
Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.;
J. Biol. Chem. 272:18827-18833(1997).
[10]
PROCESSING.
PubMed-9427603;
Tanaka M., Itoi T., Adachi M., Nagata S.;
Downregulation of Fas ligand by shedding.;
Nat. Med. 4:31-36(1998).
-!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
transduces the apoptotic signal into cells. May be involved in
cytotoxic T cell mediated apoptosis and in T cell development.
TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
peripheral tolerance, in the antigen-stimulated suicide of mature
T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
modulates its effects.
-!- SUBUNIT: HOMOPRIMER (PROBABLE).
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
SURFACE.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2;
are produced by alternative splicing.
-!- PTM: N-glycosylated.
-!- PTM: The soluble form derives from the membrane form by
proteolytic processing.
-!- DISEASE: defects in TNFRSF6 are a cause of autoimmune
lymphoproliferative syndrome (ALPS), also known as Canale-Smith
syndrome (CSS), a childhood syndrome involving hemolytic anemia
and thrombocytopenia with massive lymphadenopathy and
splenomegaly.
-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/3338769674.g.htm".

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or send an email to license@isb-sib.ch).

EMBL; X89102; CAA61474.1; -
EMBL; U08137; AAC50071.1; -
EMBL; U11821; AAC50124.1; -
EMBL; D38122; BAA07320.1; -
EMBL; AF288573; AAG60017.1; -
EMBL; Z36050; CAB09424.1; -
EMBL; BC017502; AAH17502.1; -
EMBL; AB013303; BAA32542.1; -
HSP; P01375; 1TNF.
Genew; HGNC:11936; TNFSF6.
MIM; 134638; -
MIM; 601859; -
InterPro; IPR003636; TNF_ab.
InterPro; IPR000478; TNF_family.

Search completed: April 16, 2003, 12:18:59
Job time : 10.5 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	263.5	15.7	214	13 Q9DD25	Q9ad25 brachydanio
2	217.5	13.0	287	13 Q9OWT9	Q9OWt9 gallus gall
3	149	8.9	234	6 Q9TTJ3	Q9ttj3 equus caball
4	142	8.5	232	4 Q9UIV3	Q9uiv3 homo sapien
5	135.5	8.0	215	11 Q9VND1	Q9vnd1 tamiasciuru
6	133	7.9	157	4 Q43647	Q43647 homo sapien
7	132	7.9	149	6 Q97543	Q97543 aotus nancy
8	132	7.9	127	11 Q9ER66	Q9erg6 peromyscus
9	131.5	7.9	156	11 Q9IZL4	Q9izl4 sigmodon hi
10	131	7.8	149	6 Q97538	Q97538 aotus vocif
11	131	7.8	149	6 Q9TIG8	Q9ttg8 aotus nigri
12	130	7.8	216	11 Q70332	Q70332 mesocricetu
13	127.5	7.6	217	6 Q9BEC5	Q9bec5 tenrec ecau
14	126.5	7.6	217	6 Q9BEG1	Q9beg1 bradypus tr
15	126.5	7.6	217	6 Q9BEG0	Q9beg0 cyclops di
16	126	7.5	216	6 Q9BEC9	Q9bec9 ochotona pr

Qy 170 NAASIPS-----GSHKVTLSWYHEDRGWAKISNMVTLNGLKRVNODGFYIL 215
 Db 56 SSASDNRSPQSDMEHPQDFLQSCRPVHTWANKSPGALHLYNMTLTNGLRVPODGRYIL 115
 Qy 216 YANICFRHHETSGVPTDYQLAVTV--KTSIKIPSHNLMKGGSTKNNSGSEFHYFS 273
 Db 116 YSQYFYRPSFSDQSSVSHQLVQCYYKTSYLNPI--QLLKGVGKWCWAPDAEYALHS 173
 Qy 274 INVGEFKLRAGEISIQVSNPSLLDPDQATYFGAKV 312
 Db 174 VTQGLFELRAGDEVFVSSTVAYGEDSSSYEGAPRL 212

RESULT 2
 Q9WT9 ID Q9WT9 PRELIMINARY; PRT; 287 AA.
 AC Q9WT9;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE TNF-related apoptosis inducing ligand.
 DE Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bridgman J.T., Johnson A.L.;
 RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
 ovary";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY057941; AAL23702.1;
 DR InterPro: IPR003636; TNF_family.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR ProDom: PD002012; TNF_abc; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 SQ SEQUENCE 287 AA; 32092 MW; DB06ELC95087B108 CRC64;

Query Match 13.08; Score 217.5; DB 13; Length 287;
 Best Local Similarity 26.78; Pred. No. 5.4e-11;
 Matches 66; Conservative 51; Mismatches 103; Indels 27; Gaps 8;

Qy 81 SEDSTHCFYRILRHENAGLDSTLESDDLPSDCRRMKQAFQAGVOKELQHVGPQRS 140
 Db 51 SSELRLCLQLNQOEGSNLEE--LISN----QSLKLANIKAYATVENVISRSVN 104
 Qy 141 GAPAMGEGWLDVAQ---RGKPEAQPFALHTI---NAASIPSG-----SHKVTLSW 186
 105 EA---QKSYENISEGQVATKLGKPSAHLIFRPNQPAQDGSRRFRGNLSQSCRHAITRW 160
 Qy 187 YHRCWAKISNMTLSNGLRVNODGFYLYANICFRHHETSGSVPTDYQLAVTV-VKTS 245
 Db 161 EDSTHSLQNTTIDGRLRNQAGKYVYSQIYFRSDGAGARVSPQDVQCNKRTS 220
 Qy 246 IKIPSHNLMKGGSTKNNSGSEFHYFSINVGGFKLRAGEISIQVSNPSLLDPDQAT 305
 Db 221 YSQPIL--LLKGVGKWCWAPAEYGLHALYOGGLFELKAGDELFSVSSLAIDYSDAAS 278
 Qy 306 YFGAKV 312
 Db 279 YFGAPRL 285

RESULT 3
 Q9TJT3 ID Q9TJT3 PRELIMINARY; PRT; 234 AA.
 AC Q9TJT3;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Tumor necrosis factor-alpha.

GN TNFA.
 OC Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OC NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPRAIN-THOROUGHRED; TISSUE-ARTERIAL ENDOTHELIUM;
 RA Ishida N., Sato F., Hasegawa T.;
 RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB035735; BAA88349.1;
 DR HSSP: P01375; IABM.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 SQ SEQUENCE 234 AA; 25430 MW; 2384D4950A21F377 CRC64;

Query Match 8.98; Score 149; DB 6; Length 234;
 Best Local Similarity 24.18; Pred. No. 4.1e-05;
 Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

Qy 133 IVGPQRSCGAPAMGEGWLDVAQRCK-----PEAQPFALHTINAASIPSGSHKVTLSWY 187
 Db 55 VIGPQREELPNAPQ--SINPLAQLRSSRTPSKPVARVAVN-----PQAEQL---QWL 106
 Qy 188 HDRGWAKISN-MTLSNGLRVNODGFYLYANICFRHHETSGSVPTDYQLAVTVVKTSL 246
 Db 107 SGRNALLANGVLTDLNQLVPLDGLYLIYSQVLEK---GGCSTHVLHTHTSLAV 162
 Qy 247 KIPSHNLMKG-----GSKNWSGSEFHYFSINVGGFKLRAGEISIQVSN 294
 Db 163 SYPSKVNLLSAIKSLANTSPQAEAKPW-----YEPYLVGGVQLEKGPOLSAEINQ 215
 Qy 295 PSLLD-PDQATYFG 308
 Db 216 PNYLDFAESGGQVYFG 230

RESULT 4
 Q9UIV3 ID Q9UIV3 PRELIMINARY; PRT; 232 AA.
 AC Q9UIV3;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Tumor necrosis factor.
 GN TNF.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93272029; PubMed-8499947;
 RA Iris F., Boudieret L., Prieur S., Caterina D., Primas G., Perrot V.,
 RA Jurka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.;
 RT "Dense Alu clustering and a potential new member of the NFkappaB
 family within a 90 kilobase HLA class III segment";
 RL Nat. Genet. 3:137-145(1993).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE-96215741; PubMed-8629302;
 RA Utans U., Quist W.C., McManus B.M., Wilson J.E., Arcese R.J.,
 RA Wallace A.F., Russell M.E.;
 RT "Allograft inflammatory factor-1. A cytokine-responsive macrophage
 molecule expressed in transplanted human hearts";
 RL Transplantation 61:1387-1392(1996).

[3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96006565; PubMed-7590964;
 RA Holzinger I., de Baey A., Messer G., Kick G., Zwierzina H.,
 RA Weiss E.H.;
 RT "Cloning and genomic characterization of LST1: a new gene in the human
 RT TNF region.";
 RL Immunogenetics 42:315-322(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93208881; PubMed-7916655;
 RA Browning J.L., Ngam-ek A., Lawton P., Demarinis J., Tizard R.,
 RA Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;
 RT "Lymphotoxin-beta: A new member of the TNF family that forms a
 RT heteromeric complex with lymphotoxin on the cell surface.";
 RL Cell 72:847-856(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86016093; PubMed-2995927;
 RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D., Jarrett-Nedwin J.,
 RA Pennica D., Goeddel D.V., Gray P.W.;
 RT "Human lymphotoxin and tumor necrosis factor genes: structure,
 RT homology and chromosomal localization.";
 RL Nucleic Acids Res. 13:6361-6373(1985).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91086846; PubMed-1670638;
 RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,
 RA Riethmuller G., Weiss E.H.;
 RT "Polymorphic Structure of the Tumor Necrosis Factor (TNF) Locus: An
 RT Ncol Polymorphism in the First Intron of the Human TNF-beta Gene
 RT Correlates with a Variant Amino Acid in Position 26 and a Reduced
 RT Level of TNF-beta Production.";
 RL J. Exp. Med. 173:209-219(1991).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91139175; PubMed-1671667;
 RA Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
 RT "Haplotypic polymorphisms of the TNFB gene.";
 RL Immunogenetics 33:50-53(1991).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94362679; PubMed-8081366;
 RA Albertella M.R., Campbell D.R.;
 RT "Characterization of a novel gene in the human major
 RT histocompatibility complex that encodes a potential new member of the
 RT I kappa B family of proteins.";
 RL Hum. Mol. Genet. 3:793-799(1994).
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95324911; PubMed-7601445;
 RA Peelman L., Chardon P., Nunes M., Renard C., Geffrotin C., Valman M.,
 RA Van Zeveren A., Coppieters W., Van de Weghe A., Bouquet Y., Choy W.,
 RA Strominger J., Spies T.;
 RT "The BAT1 Gene in the MHC Encodes an Evolutionarily Conserved Putative
 RT Nuclear RNA Helicase of the D-E-A-D Family.";
 RL Genomics 26:210-218(1995).
 RN [10]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20132445; PubMed-10668961;
 RA Neville M.J., Campbell R.D.;
 RT "Alternative splicing of the LSP-1 gene located in the major
 RT histocompatibility complex on human chromosome 6.";
 RL DNA Seq. 8:155-160(1997).
 RN [11]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98035883; PubMed-9367684;
 RA de Baey A., Fellerhoff B., Maier S., Martinuzzi S., Weidle U.,
 RA Weiss E.H.;
 RT "Complex expression pattern of the TNF region gene LST1 through
 RT differential regulation, initiation, and alternative splicing.";
 RL Genomics 45:591-600(1997).
 RN [12]

RP SEQUENCE FROM N.A.
 RX MEDLINE-98149985; PubMed-9480751;
 RA Shida T., Tamiya G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,
 RA Goto K., Mizuki N., Watanabe K., Fukuzumi Y., Taguchi S., Sugawara C.,
 RA Ono A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,
 RA Kimura M., Inoko H.;
 RT "Nucleotide sequencing analysis of the 146-kilobase segment around the
 RT IKBL and MICA genes at the centromeric end of the HLA class I
 RT region.";
 RL Genomics 47:372-382(1998).
 DR EMBL: Y14769; CAA75070.1; --
 DR HSP; P01375; 4TSV.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR PRODOM: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 SQ SEQUENCE 232 AA; 25446 MW; E4D71B19C6AE0D03 CRC64;
 Query Match 8.5%; Score 142; DB 4; Length 232;
 Best Local Similarity 24.5%; Pred. No. 0.00017;
 Matches 48; Conservative 37; Mismatches 69; Indels 42; Gaps 11;
 QY 133 IVGPQR--FSGAPAMEGSLDVAQRGK----PEAQPFAHLTINAAIPSGSHKVTLSW 186
 DB 55 VIGPQREFFRDLISLIS----PLAAGSSRSRTPSDKPAHVAVN----PQAEGL---QW 103
 QY 187 YHGRGWAQISN-MTSLNGKLRVNDGFFLYANICFRHETSGSVPTDYQLQ----- 237
 DB 104 LRRANALLANGVELRDNLVVPSEGLYLYSQVLFK----GQCSTHVLITHTISRIA 159
 QY 238 MVYVVK-----TSIKIPSSHNLKGGSTKNMGNSSEFFHYISVNGGFKLRAGEISIQVS 293
 DB 160 VSYQTKVNLISAIKSPQRETPEGAERPW-----YEPYLGQVQLKGRDLRSAIN 212
 QY 294 NPSLLD-PDQATYFG 308
 DB 213 RPYLDFAESGQVYFG 228
 RESULT 5
 Q99ND1 ID Q99ND1 PRELIMINARY; PRT; 215 AA.
 AC Q99ND1;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Tumor necrosis factor (Fragment).
 GN TNFA.
 OS Tamiasciurus hudsonicus (American red squirrel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Tamiasciurus
 OC NCBI_TaxID=10009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA van Dijk M.A.M., de Jong W.W.;
 RT "Indels indicate that rodents are monophyletic and lagomorphs are
 RT their sister group.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ286824; CAC28340.1; --
 DR HSP; P06804; 2TNF.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR PRODOM: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.

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FT NON_TER 1 1
FT NON_TER 215 215
SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;

Query Match 8.0%; Score 133.5; DB 11; Length 215;
Best Local Similarity 24.3%; Pred. No. 0.00083;
Matches 45; Conservative 30; Mismatches 71; Indels 39; Gaps 7;

QY 133 IVGPORF---SCAPAMGSLDVAQRGK-PEAQPFAHLTINAASIPSGSHKVTLSWTH 188
DB 46 VIGPQREPPNPLPSAQAQMLTRSSQNMNDKPAHVAVNQT-----EQQLWLS 97

QY 189 DRGWAKISN-MTSLNGKLRVNODGYIYANICFRHETSGSVPTDYIQLMYVYVK---- 243
DB 98 RRANALLANGMELIDNQLWVPADGLYIYQVLFQGGCSTV-----LLHTVTSRFAV 151

QY 244 -----TSKIPSSHNLKMGSTKNSGSEHFYSINVGFFKLKPAGEEISIQVSN 294
DB 152 SYODKVNLLSAIKSPCKESLEGAEPKPM-----YEPYLGGVFLEKQGRLSAEVNL 204

QY 295 PSLLD 299
DB 205 PSYLD 209

RESULT 6
Q43647 PRELIMINARY; PRT; 157 AA.
AC Q43647;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DE 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
CN TNFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043342; AAC03542.1; -
DR HSSP; P01375; IAGM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 157 AA; 17380 MW; D13448222679F20 CRC64;

Query Match 7.9%; Score 133; DB 4; Length 157;
Best Local Similarity 24.4%; Pred. No. 0.0006;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

QY 159 PEAQPPAHLTINAASIPSGSHKVTLSWTHDRGWAKISN-MTSLNGKLRVNODGYIYLA 217
DB 8 PSDKPPAVHVAN---PQAEGL---QWLNRRANALLANGVELRDNLQVPSSEGLYIYS 60

QY 218 NICEFRHETSGSVPTDYIQL-----MVYVVK-----TSIKIPSSHNLKMGSTKNWSG 265
DB 61 QVLFK----GQCCPSTHLLTHTISRIAVSYQTKVLLSAIKSPCORETPGAEAKPW-- 114

QY 266 NSEFHYISNVGFFKLKPAGEEISIQVSNPSLLD-PDQDATYFG 308
DB 115 -----YEPYLGGVFLEKQGRLSAEINRPDYLDFAESGVYFG 153

RESULT 7
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Q97543
ID Q97543 PRELIMINARY; PRT; 149 AA.
AC Q97543;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus nancymae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
RT Identification, cloning and sequencing of different interleukin genes in 4 Aotus species.
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014513; AAD01539.1; -
DR HSSP; P01375; WTSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFABA CRC64;

Query Match 7.9%; Score 132; DB 6; Length 149;
Best Local Similarity 24.4%; Pred. No. 0.00068;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

QY 159 PEAQPPAHLTINAASIPSGSHKVTLSWTHDRGWAKISN-MTSLNGKLRVNODGYIYLA 217
DB 1 PSDKPPAVHVAN---PQAEGL---QWLNRRANALLANGVELRDNLQVPSSEGLYIYS 53

QY 218 NICEFRHETSGSVPTDYIQL-----MVYVVK-----TSIKIPSSHNLKMGSTKNWSG 265
DB 54 QVLFK----GQCCPSTHLLTHTISRIAVSYQTKVLLSAIKSPCORETPGAEAKPW-- 107

QY 266 NSEFHYISNVGFFKLKPAGEEISIQVSNPSLLD-PDQDATYFG 308
DB 108 -----YEPYLGGVFLEKQGRLSAEINRPDYLDFAESGVYFG 146

RESULT 8
Q9ERG6 PRELIMINARY; PRT; 217 AA.
AC Q9ERG6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor necrosis factor genes."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307013; RAG30264.1; -
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
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[illegible]

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DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match
Best Local Similarity 24.4%; Score 131; DB 6; Length 149;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

OY 159 PEAQPAHLTINAASIPSGSHKVTLSWYHGRWAKISN-MTSLNGKLRVNDGFFYLVA 217
DB 1 PSDKPVAHVAN---PQAEGL---QWLNRRANALLANGVELRDNQLVVPSEGLYLVS 53
218 NICFRHETSGVPTDYQL-----MYVVK-----TSIKIPSSHNLKMGSTKNWSG 265
54 QVLFK-----GQCSTFTMLLTHSIRIAVSYQAKVNLSSAIKSPQOREPFRGAKTNPW-- 107
266 NSEPHFYSINVGFFKLRAGEISIQVSNPSLLD-PDQDATYFG 308
108 -----YEPYLGGVFQLEKGRDLSAEINLPDYLDLAESQVYFG 146

RESULT 12
ID 070332 PRELIMINARY; PRT; 216 AA.
AC 070332;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RX MEDLINE=98233404; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
FT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
leishmaniasis."
L Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046215; AAC40100.1; -.
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 23793 MW; BADA3F8F345B533 CRC64;

Query Match
Best Local Similarity 24.7%; Score 130; DB 11; Length 216;
Matches 46; Conservative 29; Mismatches 71; Indels 40; Gaps 8;

OY 133 IVGPORFSGAPAMGSGWLDV-----AQRKPEAQPAHLTINAASIPSGHKVTLIS-SWY 187
DB 47 VIGPQREKFPNPIIGSGMQTLTLRSSSSQNSDKPGVHYVAN-----HQVEQLEWL 98

us-09-787-126-4.rspt
OY 188 HDRGWAKISN-MTSLNGKLRVNDGFFYLVAICFRHETSGVPTDYQLQMLVYVVK--- 243
DB 99 SHRANALLANGSLKDNQVLPADGLYLYVSQVLFER-----GQCPSIV-LLTHVSRIA 152
OY 244 -----TSIKIPSSHNLKMGSTKNWSGSEPHFYSINVGFFKLRAGEISIQVS 293
DB 153 VSYEDVNLSSAIKSPCKRTPPEGEELPW-----YEPYLGGVFQLEKGRDLSAEVN 205
OY 294 NPSLLD 299
DB 206 LPKYLD 211

RESULT 13
OYBEC5 PRELIMINARY; PRT; 217 AA.
ID OYBEC5
AC OYBEC5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Tenrec ecaudatus (tailless tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Tenrec.
OX NCBI_TaxID=94439;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286826; CAC28538.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 217
SQ SEQUENCE 217 AA; 23845 MW; 1C5013EB9B77B54A CRC64;

Query Match
Best Local Similarity 24.0%; Score 127.5; DB 6; Length 217;
Matches 49; Conservative 29; Mismatches 51; Indels 75; Gaps 10;

OY 133 IVGPORFSGAPAMGSGWLDVVAQRKPEAQ-----PFAHLTINAASIPSGSIK 180
DB 46 VIGPQREKQFP-----GSFHLI-----KPLTQTLRSSRSLSDKPVAVHW--ASTQDEGQLK 95
OY 181 VTLSSWYHGRGW-AKISNMTLSN-----GKLRVNDGFFYLVAICFRHETSGVPTD 233
DB 96 -----WVSRVANALLDNVQLDNLVPLDGLYLYVSQVLFKPGCHGT----- 140
OY 234 YLQMLVYVVK-----SIKIPSSHNLKMGSTKNWSGSEPHFYSIN 275
DB 141 -----YVLTHTVSRVIAVSYQAKVNLSSAIKTPCHRETPESETKPW-----YEPY 187
OY 276 VGGFKLRAGEISIQVSNPSLLD 299
DB 188 LGGVFQLEKGRDLSAEINLPNYLD 211

RESULT 14
OYBEC1 PRELIMINARY; PRT; 217 AA.
ID OYBEC1
AC OYBEC1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)

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01-JUN-2001 (Tremblrel. 17, Last sequence update)
01-DEC-2001 (Tremblrel. 19, Last annotation update)
Tumor necrosis factor (Fragment).
TNFA.
OS Bradypus tridactylus (Pale-throated three-toed sloth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Bradypodidae; Bradypus.
OX NCBI_TaxID=9354;
RN [1]
SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RP "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286827; CAC28513.1;
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
JR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23655 MW; A7056710B6238074 CRC64;
Query Match 7.6%; Score 126.5; DB 6; Length 217;
Best Local Similarity 25.0%; Pred. No. 0.0035;
Matches 47; Conservative 33; Mismatches 65; Indels 43; Gaps 10;
QY 133 IVGPORFGAPAMGGWNL--DVAQRGK-----PEAQFAHLTINAASIPSGSHKVTLS 185
DB 46 VIGPQREEQFP--DGLHLLSPLAQLTRSSSRTPSDKPVARVVAN---PQAEGL---Q 95
QY 186 WYDRGWAKISN-MTSLNGKLRVNDGFYLYANICFRHETSGSVPTDYQLMYYVVK- 243.
DB 96 WLSRRANALLANGVELDNLQVPSDGLYLYSQVLFK-GGCGFSTPV---LTHVNR 150
QY 244 -----TSIKIPSSHNLKMGSTKNWGNSEFHFYSINVGFFKLRAEEISIQ 291
DB 151 FAVSVQTKVNLSSAIKSPCQRETPEGTEGKPV-----YEPYLGGVFQLDKGRLSAE 203
QY 292 VSNFSLLD 299
DB 204 INLPDYLD 211
RESULT 15
QYBEGO QYBEGO PRELIMINARY; PRF; 217 AA.
AC QYBEGO;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Cyclopes didactylus (silky anteater).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.
OX NCBI_TaxID=84074;
RN [1]
SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RP "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286828; CAC28514.1;
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.

DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23753 MW; F760E887F6C29EBB CRC64;
Query Match 7.6%; Score 126.5; DB 6; Length 217;
Best Local Similarity 24.9%; Pred. No. 0.0035;
Matches 46; Conservative 33; Mismatches 69; Indels 37; Gaps 10;
QY 133 IVGPQ--RESGA--PAMMEGSLDVAQRGKPEAQFAHLTINAASIPSGSHKVTLSWY 187
DB 46 VIGPQEEQFRGGLHPVNPPLAQLTRSSSRTPSDKPVARVVAN---PQAEGL---QWL 97
QY 188 HDRGWAKISN-MTSLNGKLRVNDGFYLYANICFRHETSGSVPTDYQL------M 238
DB 98 SRRANALLANGVELDNLQVPSDGLYLYSQVLFK-----GGCGPSARVLLTHVNRPAV 153
QY 239 VYVVK-----TSIKIPSSHNLKMGSTKNWGNSEFHFYSINVGFFKLRAEEISIQVSN 294
DB 154 SYQTKVNLSSAIKSPCQRETPEGTEGKPV-----YEPYLGGVFQLDKGRLSAEINL 206
QY 295 PSLLD 299
DB 207 PEYLD 211
Search completed: April 16, 2003, 12:20:03
Job time : 30 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1675	100.0	316	2	US-08-842-842-7	Sequence 7, Appl
2	1675	100.0	316	4	US-08-989-362-2	Sequence 2, Appl
3	1675	100.0	316	4	US-09-052-521C-2	Sequence 2, Appl
4	1554	92.8	294	3	US-08-996-139-11	Sequence 11, Appl
5	1554	92.8	294	4	US-08-995-659-11	Sequence 11, Appl
6	1554	92.8	294	4	US-09-215-649A-11	Sequence 11, Appl
7	1554	92.8	294	4	US-09-577-780-11	Sequence 11, Appl
8	1417.5	84.6	317	3	US-08-996-139-13	Sequence 13, Appl
9	1417.5	84.6	317	4	US-08-995-659-13	Sequence 13, Appl
10	1417.5	84.6	317	4	US-09-215-649A-13	Sequence 13, Appl
11	1417.5	84.6	317	4	US-09-052-521C-4	Sequence 4, Appl
12	1417.5	84.6	317	4	US-09-577-780-13	Sequence 13, Appl
13	258.5	15.4	279	4	US-09-072-993C-3	Sequence 3, Appl
14	258.5	15.4	281	1	US-08-670-354-2	Sequence 2, Appl
15	258.5	15.4	281	3	US-08-584-031-1	Sequence 1, Appl
16	258.5	15.4	281	3	US-08-780-496-1	Sequence 1, Appl
17	258.5	15.4	281	4	US-08-883-086-10	Sequence 10, Appl
18	258.5	15.4	281	4	US-09-320-424-2	Sequence 2, Appl
19	258.5	15.4	281	4	US-09-333-593A-6	Sequence 6, Appl
20	258.5	15.4	281	4	US-09-157-864-11	Sequence 11, Appl
21	258.5	15.4	281	5	PCT-US96-10895-2	Sequence 2, Appl
22	244	14.6	291	1	US-08-670-354-6	Sequence 6, Appl
23	244	14.6	291	4	US-09-320-424-6	Sequence 6, Appl
24	244	14.6	291	5	PCT-US96-10895-6	Sequence 6, Appl
25	240	14.3	256	4	US-09-320-424-13	Sequence 13, Appl
26	236	14.1	253	4	US-09-320-424-11	Sequence 11, Appl
27	229.5	13.7	177	4	US-09-105-343A-7	Sequence 7, Appl

QY 181 VTLSWYHNRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHHTSGSVPTDYQLQVY 240
DB 181 VTLSWYHNRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHHTSGSVPTDYQLQVY 240
QY 241 VVTSIKIPSSHNLMKGGSTKNWSEPHFYSINVGFFKLRAGEEISIQVSNPSLLDP 300
DB 241 VVTSIKIPSSHNLMKGGSTKNWSEPHFYSINVGFFKLRAGEEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVQDID 316
DB 301 DQDATYFGAFKVQDID 316

RESULT 2
US-08-989-362-2
; Sequence 2, Application US/08989362
; Patent No. 6242586
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
; TITLE OF INVENTION: Regents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,362
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 56
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,846
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0686
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-989-362-2

Query Match 100.0%; Score 1675; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.7e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYKYLRSSEMGSGPGVPHGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
DB 1 MRRASRDYKYLRSSEMGSGPGVPHGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
QY 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESDTLPDSCRMKQ 120
DB 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESDTLPDSCRMKQ 120
QY 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRGKPEAOPFAHLTTNAASIPSGSHK 180
DB 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRGKPEAOPFAHLTTNAASIPSGSHK 180

QY 181 VTLSWYHNRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHHTSGSVPTDYQLQVY 240
DB 181 VTLSWYHNRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHHTSGSVPTDYQLQVY 240
QY 241 VVTSIKIPSSHNLMKGGSTKNWSEPHFYSINVGFFKLRAGEEISIQVSNPSLLDP 300
DB 241 VVTSIKIPSSHNLMKGGSTKNWSEPHFYSINVGFFKLRAGEEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVQDID 316
DB 301 DQDATYFGAFKVQDID 316

RESULT 3
US-09-052-521C-2
; Sequence 2, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PPT
; ORGANISM: Mouse
US-09-052-521C-2

Query Match 100.0%; Score 1675; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.7e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYKYLRSSEMGSGPGVPHGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
DB 1 MRRASRDYKYLRSSEMGSGPGVPHGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
QY 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESDTLPDSCRMKQ 120
DB 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESDTLPDSCRMKQ 120
QY 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRGKPEAOPFAHLTTNAASIPSGSHK 180
DB 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRGKPEAOPFAHLTTNAASIPSGSHK 180
QY 181 VTLSWYHNRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHHTSGSVPTDYQLQVY 240
DB 181 VTLSWYHNRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHHTSGSVPTDYQLQVY 240
QY 241 VVTSIKIPSSHNLMKGGSTKNWSEPHFYSINVGFFKLRAGEEISIQVSNPSLLDP 300
DB 241 VVTSIKIPSSHNLMKGGSTKNWSEPHFYSINVGFFKLRAGEEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVQDID 316
DB 301 DQDATYFGAFKVQDID 316

RESULT 4
US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene

```

; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-996-139-11

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Query Match          92.8%; Score 1554; DB 3; Length 294;
Best Local Similarity 99.7%; Pred. No. 3.5e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 23 GYPHEGLHPAPSAPAPAPPAAASRSMFLALIGLGQVVCISIALFLYFRAQMDPNRISE 82
Jb 1 GYPHEGLHPAPSAPAPAPPAAASRSMFLALIGLGQVVCISIALFLYFRAQMDPNRISE 60
Qy 83 DSTHCFYRLRLHENAGLDSTLESDTLPSCRMKQAFQAVOKELQHVGPORFSGA 142
Db 61 DSTHCFYRLRLHENAGLDSTLESDTLPSCRMKQAFQAVOKELQHVGPORFSGA 120
Qy 143 PAMBGSLDVAQRKPEAQPPFAHLTINAAISPSGSHKVTLSWYHDRGWAKISNMTLSN 202
Db 171 PAMBGSLDVAQRKPEAQPPFAHLTINAAISPSGSHKVTLSWYHDRGWAKISNMTLSN 180
Qy 203 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMIVYVVKTSIKIPSSHNLMKGGSTKN 262
Db 181 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMIVYVVKTSIKIPSSHNLMKGGSTKN 240
Qy 263 WSGNSEFHYSINWGGFFKLRAGEISIQVSNPSLLDDPDODATYFGAFKVQDID 316
Db 241 WSGNSEFHYSINWGGFFKLRAGEISIQVSNPSLLDDPDODATYFGAFKVQDID 294

RESULT 5
US-08-995-659-11
; Sequence 11, Application US/08995569
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.

```

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; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-995-659-11

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Query Match          92.8%; Score 1554; DB 4; Length 294;
Best Local Similarity 99.7%; Pred. No. 3.5e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 23 GYPHEGLHPAPSAPAPAPPAAASRSMFLALIGLGQVVCISIALFLYFRAQMDPNRISE 82
Db 1 GYPHEGLHPAPSAPAPAPPAAASRSMFLALIGLGQVVCISIALFLYFRAQMDPNRISE 60
Qy 83 DSTHCFYRLRLHENAGLDSTLESDTLPSCRMKQAFQAVOKELQHVGPORFSGA 142
Db 61 DSTHCFYRLRLHENAGLDSTLESDTLPSCRMKQAFQAVOKELQHVGPORFSGA 120
Qy 143 PAMBGSLDVAQRKPEAQPPFAHLTINAAISPSGSHKVTLSWYHDRGWAKISNMTLSN 202
Db 121 PAMBGSLDVAQRKPEAQPPFAHLTINAAISPSGSHKVTLSWYHDRGWAKISNMTLSN 180
Qy 203 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMIVYVVKTSIKIPSSHNLMKGGSTKN 262
Db 181 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMIVYVVKTSIKIPSSHNLMKGGSTKN 240
Qy 263 WSGNSEFHYSINWGGFFKLRAGEISIQVSNPSLLDDPDODATYFGAFKVQDID 316
Db 241 WSGNSEFHYSINWGGFFKLRAGEISIQVSNPSLLDDPDODATYFGAFKVQDID 294

RESULT 6

```

US-09-215-649A-11

; Sequence 11, Application US/09215649A
; Patent No. 6271349

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/215,649A

FILING DATE: 17-Dec-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139

FILING DATE: <Unknown>

APPLICATION NUMBER: USN 08/913,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2851-A

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 294 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-215-649A-11

Query Match 92.8%; Score 1554; DB 4; Length 294;
Best Local Similarity 99.7%; Pred. No. 3.5e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	23	GVPEHGLHPAPAPAPPPAASRSMTLLGLGLGVVCSIALFLYFRAQMDPNRISE	82
Db	1	GVPEHGLHPAPAPAPPPAASRSMTLLGLGLGVVCSIALFLYFRAQMDPNRISE	60
QY	83	DSTHCFYRIILRLHENAGLDSTLESDTLPDSCRRMKQAFQGVQKLOHIVGQRFSGA	142
Db	61	DSTHCFYRIILRLHENAGLDSTLESDTLPDSCRRMKQAFQGVQKLOHIVGQRFSGA	120
QY	143	PAMMEGSLDVAQGRPEAQPFAHLITINAAIPSGSHKVTLSWYHWRGAKISNMTLSN	202
Db	121	PAMMEGSLDVAQGRPEAQPFAHLITINAAIPSGSHKVTLSWYHWRGAKISNMTLSN	180
QY	203	GKLRVNDGYYLYANICFRHETSGSVPTDYQLQVMYVYVVKTSIKIPSSHNLMKGGSTKN	262
Db	181	GKLRVNDGYYLYANICFRHETSGSVPTDYQLQVMYVYVVKTSIKIPSSHNLMKGGSTKN	240
QY	263	WGSNSFHYTSINVGGFFKLAGEEISIQVSNPDLDPQDQATYFGAFKQVODID	316
Db	241	WGSNSFHYTSINVGGFFKLAGEEISIQVSNPDLDPQDQATYFGAFKQVODID	294

RESULT 7

US-09-577-780-11

; Sequence 11, Application US/09577780

; Patent No. 6419929

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/577,780

FILING DATE: 24-May-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: <Unknown>

APPLICATION NUMBER: USN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 294 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-577-780-11

Query Match 92.8%; Score 1554; DB 4; Length 294;
Best Local Similarity 99.7%; Pred. No. 3.5e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	23	GVPEHGLHPAPAPAPPPAASRSMTLLGLGLGVVCSIALFLYFRAQMDPNRISE	82
Db	1	GVPEHGLHPAPAPAPPPAASRSMTLLGLGLGVVCSIALFLYFRAQMDPNRISE	60
QY	83	DSTHCFYRIILRLHENAGLDSTLESDTLPDSCRRMKQAFQGVQKLOHIVGQRFSGA	142
Db	61	DSTHCFYRIILRLHENAGLDSTLESDTLPDSCRRMKQAFQGVQKLOHIVGQRFSGA	120
QY	143	PAMMEGSLDVAQGRPEAQPFAHLITINAAIPSGSHKVTLSWYHWRGAKISNMTLSN	202
Db	121	PAMMEGSLDVAQGRPEAQPFAHLITINAAIPSGSHKVTLSWYHWRGAKISNMTLSN	180
QY	203	GKLRVNDGYYLYANICFRHETSGSVPTDYQLQVMYVYVVKTSIKIPSSHNLMKGGSTKN	262
Db	181	GKLRVNDGYYLYANICFRHETSGSVPTDYQLQVMYVYVVKTSIKIPSSHNLMKGGSTKN	240
QY	263	WGSNSFHYTSINVGGFFKLAGEEISIQVSNPDLDPQDQATYFGAFKQVODID	316
Db	241	WGSNSFHYTSINVGGFFKLAGEEISIQVSNPDLDPQDQATYFGAFKQVODID	294

Query Match	84.6%	Score 1417.5	DB 3	Length 317
Best Local Similarity	84.3%	Pred. No. 1.le-131		
Matches 268	Conservative 16	Mismatches 31	Indels 3	Gaps 2
QY	1	MRRASRDYGKYLRSSEEMSGPGVHEGPHLPAPSAPAPAPPPASRSMFTALLGLGLGQ	60	
Db	1	MRRASRDYTKLRSSEEMSGGPGAPHEGPHL-APPPAPHPGPPASRSMFTALLGLGLGQ	59	
QY	61	VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLDSTLESBDT--LPDSCRRM	118	
Db	60	VVCSVALFFYFRAQMDPNRISEDCTHCFYRILRLHENADFQDTTLESQDTKLIPDSCRR	119	
QY	119	KQAPQGAQVQELQHVIGVQRFSGAPAMWEGSWLDVAQBGKPEAQPFALHTTNASIPSGS	178	
Db	120	KQAPQGAQVQELQHVIGVQSHIRAEKAMVDGSWLDLAKSKLEAQPFALHTTNATDIPSGS	179	
QY	179	HKVLSLWYHDRGWAKTSNMTLNGLKRVNODGFYIYANICFRHHETSGSVPTDYQLQM	238	
Db	180	HKVLSLWYHDRGWAKTSNMTFNGLKRVNODGFYIYANICFRHHETSGDLAEYQLQM	239	
QY	239	VYVVKTSIKIPSSHNLKMGGSTKNWGNSEPHFYSINVGGFFKLURAGEEISIQVSNPSLL	298	

Query Match 84.6%: Score 1417.5: DB 4: Length 317:

Db 120 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAQPFALHTINATDIPSGS 179
 QY 179 HKVTLSSYHDSRGWAKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYQLM 238
 Db 180 HKVTLSSYHDSRGWAKISNMTLSNGLKRVNODGFYLLYANICFRHETSGDLATEYLQM 239
 QY 239 VYVTKTSIKIPSSHLMKGGSTKNWSEHFYISINVGFFKLRAGEEISIQVSNPSLL 298
 Db 240 VYVTKTSIKIPSSHLMKGGSTKNWSEHFYISINVGFFKLRAGEEISIEVSNPSLL 299
 QY 299 DPQDATYFGAFKVDID 316
 Db 300 DPQDATYFGAFKVRDID 317

RESULT 10

US-09-215-649A-13
 ; Sequence 13, Application US/09215649A
 ; Patent No. 6271349

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
 Galibert, Laurent
 Maraskovsky, Eugene
 TITLE OF INVENTION: Receptor Activator of NF-kappaB
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation, Law Department
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/215,649A
 FILING DATE: 17-Dec-1998
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/996,139
 FILING DATE: <Unknown>
 APPLICATION NUMBER: USSN 08/813,509
 FILING DATE: 07 MARCH 1997
 APPLICATION NUMBER: USSN 08/772,330
 FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2851-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-215-649A-13

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
 Best Local Similarity 84.3%; Pred. No. 1.1e-131;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYCKYLRSSEMGSGPGVHEGPHLPAPAPAPPAASRSMFALLGLGLGQ 60
 Db 1 MRRASRDYCKYLRSSEMGSGPGVHEGPHLPAPAPPAASRSMFALLGLGLGQ 59

QY 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRLRLHLENAGLDSTLESDT--LPDSCRM 118
 Db 60 VVCSVALFFYFRAQMDPNRISEDSHCFYRLRLHLENAGLDSTLESDT--LPDSCRM 119
 QY 119 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAQPFALHTINATDIPSGS 178
 Db 120 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAQPFALHTINATDIPSGS 179
 QY 179 HKVTLSSYHDSRGWAKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYQLM 238
 Db 180 HKVTLSSYHDSRGWAKISNMTLSNGLKRVNODGFYLLYANICFRHETSGDLATEYLQM 239
 QY 239 VYVTKTSIKIPSSHLMKGGSTKNWSEHFYISINVGFFKLRAGEEISIQVSNPSLL 298
 Db 240 VYVTKTSIKIPSSHLMKGGSTKNWSEHFYISINVGFFKLRAGEEISIEVSNPSLL 299
 QY 299 DPQDATYFGAFKVDID 316
 Db 300 DPQDATYFGAFKVRDID 317

RESULT 11

US-09-052-521C-4
 ; Sequence 4, Application US/09052521C
 ; Patent No. 6316408

GENERAL INFORMATION:

APPLICANT: Boyle, William J.
 TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
 FILE REFERENCE: A-451brv
 CURRENT APPLICATION NUMBER: US/09/052,521C
 CURRENT FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 08/880,855
 PRIOR FILING DATE: 1997-06-23
 PRIOR APPLICATION NUMBER: 08/842,842
 PRIOR FILING DATE: 1997-04-16
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 317
 TYPE: PRT
 ORGANISM: Human
 US-09-052-521C-4

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
 Best Local Similarity 84.3%; Pred. No. 1.1e-131;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYCKYLRSSEMGSGPGVHEGPHLPAPAPAPPAASRSMFALLGLGLGQ 60
 Db 1 MRRASRDYCKYLRSSEMGSGPGVHEGPHLPAPAPPAASRSMFALLGLGLGQ 59
 QY 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRLRLHLENAGLDSTLESDT--LPDSCRM 118
 Db 60 VVCSVALFFYFRAQMDPNRISEDSHCFYRLRLHLENAGLDSTLESDT--LPDSCRM 119
 QY 119 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAQPFALHTINATDIPSGS 178
 Db 120 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAQPFALHTINATDIPSGS 179
 QY 179 HKVTLSSYHDSRGWAKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYQLM 238
 Db 180 HKVTLSSYHDSRGWAKISNMTLSNGLKRVNODGFYLLYANICFRHETSGDLATEYLQM 239
 QY 239 VYVTKTSIKIPSSHLMKGGSTKNWSEHFYISINVGFFKLRAGEEISIQVSNPSLL 298
 Db 240 VYVTKTSIKIPSSHLMKGGSTKNWSEHFYISINVGFFKLRAGEEISIEVSNPSLL 299
 QY 299 DPQDATYFGAFKVDID 316
 Db 300 DPQDATYFGAFKVRDID 317

RESULT 12

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:18:42 ; Search time 14.5 seconds
(without alignments)
1647.861 Million cell updates/sec

Title: US-09-787-126-4
Perfect score: 1675
Sequence: 1 MRRASRDYKYLRSSEMGs.....LLDPQDQATYFGAKVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 288829 seqs, 75613885 residues
Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUB.pap.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	316	9	US-10-017-910-4
2	1675	100.0	316	9	US-10-105-057-2
3	1554	92.8	294	9	US-09-877-650-11
4	1554	92.8	294	10	US-09-871-856-11
5	1417.5	84.6	317	9	US-09-877-650-13
6	1417.5	84.6	317	10	US-09-813-329-7
7	1417.5	84.6	317	10	US-09-871-856-13
8	1101	65.7	245	9	US-10-017-910-2
9	855	51.0	160	9	US-09-779-050A-14
10	768	45.9	160	9	US-09-779-050A-15
11	496	29.6	109	10	US-09-911-777-8
12	258.5	15.4	279	12	US-10-066-209-3
13	258.5	15.4	281	8	US-08-916-625B-6
14	258.5	15.4	281	9	US-08-971-317A-8
15	258.5	15.4	281	9	US-10-001-054-54
16	258.5	15.4	281	9	US-10-093-766-54
17	258.5	15.4	281	9	US-10-174-654-11
18	258.5	15.4	281	9	US-10-151-882-41
19	258.5	15.4	281	10	US-09-813-329-17

20	258.5	15.4	281	10	US-09-193-663-8	Sequence 8, Appl
21	258.5	15.4	281	10	US-09-934-465-1	Sequence 1, Appl
22	258.5	15.4	281	12	US-10-039-785-66	Sequence 66, Appl
23	258.5	15.4	281	12	US-10-011-125-4	Sequence 4, Appl
24	244	14.6	291	9	US-10-017-910-6	Sequence 6, Appl
25	234	14.0	296	9	US-10-185-425-5	Sequence 5, Appl
26	232	13.9	246	10	US-09-855-544A-13	Sequence 13, Appl
27	230.5	13.8	168	10	US-09-900-530A-10	Sequence 10, Appl
28	229.5	13.7	166	9	US-09-779-050A-16	Sequence 16, Appl
29	225	13.4	172	9	US-09-779-050A-17	Sequence 17, Appl
30	220.5	13.2	164	12	US-10-116-378-29	Sequence 29, Appl
31	183	10.9	278	10	US-09-246-129B-6	Sequence 6, Appl
32	183	10.9	278	10	US-09-899-059-6	Sequence 6, Appl
33	182	10.9	279	9	US-10-017-910-5	Sequence 5, Appl
34	181	10.8	279	8	US-08-971-317A-4	Sequence 4, Appl
35	181	10.8	279	10	US-09-193-663-4	Sequence 4, Appl
36	176	10.5	87	10	US-09-880-457-4	Sequence 4, Appl
37	176	10.5	94	10	US-09-880-457-5	Sequence 5, Appl
38	176	10.5	95	9	US-10-237-884-82	Sequence 82, Appl
39	176	10.5	95	9	US-10-230-163-82	Sequence 82, Appl
40	176	10.5	95	9	US-10-218-631-82	Sequence 82, Appl
41	176	10.5	95	9	US-10-230-338-82	Sequence 82, Appl
42	176	10.5	95	9	US-10-230-414-82	Sequence 82, Appl
43	176	10.5	95	9	US-10-216-159A-82	Sequence 82, Appl
44	176	10.5	95	10	US-09-880-457-6	Sequence 6, Appl
45	173.5	10.4	281	8	US-08-971-317A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-017-910-4
; Sequence 4, Application US/10017910
; Patent No. US20020159970A1

GENERAL INFORMATION:
APPLICANT: Choi, Yongwon

Wong, Brian
Josien, Regis
Steinman, Ralph

TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCOD METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/017,910

FILING DATE: 14-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/447,035

FILING DATE: 1999-11-22

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-200

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

Oy	1	MRRASDYGKYLSRSEEMSGPGVHPBGLHPAPSA	PAPPAAKSMTALLIGLGG	60
Db	1	MRRASDYGKYLSRSEEMSGPGVHPBGLHPAPSA	PAPPAAKSMTALLIGLGG	60
Oy	61	VCSIALFLYFRAQMDPNRISEDSTHCFYRILRLI	HENAGLDSTLSEDTLPDSCRMMQ	120
Db	61	VCSIALFLYFRAQMDPNRISEDSTHCFYRILRLI	HENAGLDSTLSEDTLPDSCRMMQ	120
Oy	121	AFOGAVOKELQHIVGPORFSCAPAMMGSLWDVA	QRCKPEAQPAHILTINAAISIPSGSHK	180
Db	121	AFOGAVOKELQHIVGPORFSCAPAMMGSLWDVA	QRCKPEAQPAHILTINAAISIPSGSHK	180
Oy	181	VTLSWSYTHDRGWAKINSNMTLSNGKLRYNODGF	FYYLYANICFRHHETSGSVPTDYQLMAY	240

1
1
2
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QY	23	GVPHEGFLHPAPSA	PAPAPPPAASRSMFLALIGLGLGVCSIALFLYFRAMDPNRISE	82
Db	1	GVPHEGFLHPAPSA	PAPAPPPAASRSMFLALIGLGLGVCSIALFLYFRAMDPNRISE	60
QY	83	DSTHCFYRILRLH	ENAGLDSTLESEDTLPDSRRMKQAFQAVOKELQHVGPQPSGA	142
Db	61	DSTHCFYRILRLH	ENADLDSTLESEDTLPDSRRMKQAFQAVOKELQHVGPQPSGA	120

Db 60 VVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFDQTTLESQDTKLIPDSMRI 119
QY 119 KQAFQAVOKELQHVGPQFSCAPAMGSGWLDVAQRKPEAOPFAHLTINAAISIPSGS 178
Db 120 KQAFQAVOKELQHVGSQHRAEKAWVDGSLDLAKRSKLEAOPFAHLTINATDIPSGS 179
QY 179 HKVTLSSWYHRCWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLM 238
Db 180 HKVTLSSWYHRCWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGDLATEYLQLM 239
QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWNSGNEFHYSINVGFFKLRAGEISIQVNSPLL 298
Db 240 VYVTKTSIKIPSSHTLMKGGSTKNWNSGNEFHYSINVGFFKLRAGEISIEVNSPLL 299
QY 299 DPQDATYFAGKVRQDID 316
Db 300 DPQDATYFAGKVRDID 317

RESULT 6

US-09-813-329-7
Sequence 7, Application US/09813329
Patent No. US20020012968A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
FILE REFERENCE: D0016.0P
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patent version 3.0
SEQ ID NO 7
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-813-329-7

Query Match 84.6%; Score 1417.5; DB 10; Length 317;
Best Local Similarity 84.3%; Pred. No. 5.2e-117;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYKYLRSSEMGSGCPVHEGPHLPAPAPAPAPPAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYKYLRSSEMGSGCPVHEGPHLPAPAPAPAPPAASRSMFLALLGLGLGQ 59
QY 61 VVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFDQTTLESQDTKLIPDSMRI 119
QY 119 KQAFQAVOKELQHVGPQFSCAPAMGSGWLDVAQRKPEAOPFAHLTINAAISIPSGS 178
Db 120 KQAFQAVOKELQHVGSQHRAEKAWVDGSLDLAKRSKLEAOPFAHLTINATDIPSGS 179
QY 179 HKVTLSSWYHRCWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLM 238
Db 180 HKVTLSSWYHRCWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGDLATEYLQLM 239
QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWNSGNEFHYSINVGFFKLRAGEISIQVNSPLL 298
Db 240 VYVTKTSIKIPSSHTLMKGGSTKNWNSGNEFHYSINVGFFKLRAGEISIEVNSPLL 299
QY 299 DPQDATYFAGKVRQDID 316
Db 300 DPQDATYFAGKVRDID 317

RESULT 7

US-09-871-856-13
Sequence 13, Application US/09871856
Patent No. US20020081720A1

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-871-856-13

Query Match 84.6%; Score 1417.5; DB 10; Length 317;
Best Local Similarity 84.3%; Pred. No. 5.2e-117;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYKYLRSSEMGSGCPVHEGPHLPAPAPAPPAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYKYLRSSEMGSGCPVHEGPHLPAPAPAPPAASRSMFLALLGLGLGQ 59
QY 61 VVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFDQTTLESQDTKLIPDSMRI 119
Db 60 VVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFDQTTLESQDTKLIPDSMRI 119
QY 119 KQAFQAVOKELQHVGPQFSCAPAMGSGWLDVAQRKPEAOPFAHLTINAAISIPSGS 178
Db 120 KQAFQAVOKELQHVGSQHRAEKAWVDGSLDLAKRSKLEAOPFAHLTINATDIPSGS 179
QY 179 HKVTLSSWYHRCWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLM 238
Db 180 HKVTLSSWYHRCWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGDLATEYLQLM 239
QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWNSGNEFHYSINVGFFKLRAGEISIQVNSPLL 298
Db 240 VYVTKTSIKIPSSHTLMKGGSTKNWNSGNEFHYSINVGFFKLRAGEISIEVNSPLL 299
QY 299 DPQDATYFAGKVRQDID 316
Db 300 DPQDATYFAGKVRDID 317

RESULT 8

US-10-017-910-2
; Sequence 2, Application US/10017910
; Patent No. US20020159970A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; Wong, Brian
; Josien, Regis
; Steinman, Ralph
; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAM
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/017,910
; FILING DATE: 14-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/447,035
; FILING DATE: 1999-11-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; MOLECULE TYPE: linear
; TYPE: amino acid
; LENGTH: 245 amino acids
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
JS-10-017-910-2

Query Match 65.7%; Score 1101; DB 9; Length 245;
Best Local Similarity 84.1%; Pred. No. 2.7e-89;
Matches 206; Conservative 14; Mismatches 23; Indels 2; Gaps 1;
QY 74 QMDPNRISDTHCFYRLRLHENAAGLDSTLESDT--LPDSCRRMKAQFQAVOKELQ 131
DB 1 QMDPNRISDTHCFYRLRLHENAAGLDSTLESDT--LPDSCRRMKAQFQAVOKELQ 60
QY 132 HIVGQRFSGAPAMMEGSLDVAQKPKPAQFAHLTINAAISIPSGSHKVTLSWYHDSRG 191
DB 61 HIVGQHFRAEKAMVDGSLDLAKSKLEAQPFAHLTINATDIPSGSHKVTLSWYHDSRG 120
QY 192 WAKTNSMTLSGKLVNODGFFYLYANICFRHETSGVPTDYQLQMLVYVVTSTIKIPSS 251
DB 121 WGTISNMTFSNGKLVNODGFFYLYANICFRHETSGDLATEYLQMLVYVVTSTIKIPSS 180
QY 252 HNLAKGSGTKWNSGSEFFHSYINVGFFKLAGEEISIOVSNPSLLDPDQDATYFGAFK 311
DB 181 HTLAKGSGTKWNSGSEFFHSYINVGFFKLAGEEISIEVSNPSLLDPDQDATYFGAFK 240
QY 312 VQDID 316
DB 241 VRDID 245

RESULT 9

US-09-779-050A-14
; Sequence 14, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-14

Query Match 51.0%; Score 855; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 7e-68;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 157 GKPEAQPFALHTINAAISIPSGSHKVTLSWYHDSRGWAKISNMTLSGKLVNODGFFYLY 216
DB 1 GKPEAQPFALHTINAAISIPSGSHKVTLSWYHDSRGWAKISNMTLSGKLVNODGFFYLY 60
QY 217 ANICFRHETSGVPTDYQLQMLVYVVTSTIKIPSSHNLKMGSTKNWSGSEFFHSYINV 276
DB 61 ANICFRHETSGVPTDYQLQMLVYVVTSTIKIPSSHNLKMGSTKNWSGSEFFHSYINV 120
QY 277 GGFKLAGEEISIOVSNPSLLDPDQDATYFGAFKVQDID 316
DB 121 GGFKLAGEEISIOVSNPSLLDPDQDATYFGAFKVQDID 160

RESULT 10

US-09-779-050A-15
; Sequence 15, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-15

Query Match 45.9%; Score 768; DB 9; Length 160;
Best Local Similarity 89.9%; Pred. No. 3.2e-60;
Matches 143; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
QY 158 KPEAQPFALHTINAAISIPSGSHKVTLSWYHDSRGWAKISNMTLSGKLVNODGFFYLY 217
DB 2 KLEAQPFALHTINATDIPSGSHKVTLSWYHDSRGWAKISNMTFSNGKLVNODGFFYLY 61
QY 218 NTCFRHETSGVPTDYQLQMLVYVVTSTIKIPSSHNLKMGSTKNWSGSEFFHSYINVG 277
DB 62 NTCFRHETSGDLATEYLQMLVYVVTSTIKIPSSHTLAKGSGTKWNSGSEFFHSYINVG 121

PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100263
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/101476
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/107783
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112420
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116533
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/131294
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 09/218517
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 09/284291
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380913
PRIOR FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/866034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/882636
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: PCT/US98/18824
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/US99/00106
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/08615
PRIOR FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28634
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00376
PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/06884
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/14941
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/22031
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:15:36 ; Search time 33.5 seconds
(without alignments)

1256.931 Million cell updates/sec

Title: US-09-787-126-6

Perfect score: 1675

Sequence: 1 MRRASRDYKYLSEEMGS.....LLDPDQATYFGAFKVDID 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002.*

1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	1675	100.0	316 19	AAW83194 Human osteoprotegerin
2	1675	100.0	316 19	AAW83017 Osteoclastogenesis
3	1675	100.0	316 19	AAW59654 Amino acid sequenc
4	1675	100.0	316 20	AAW17874 Murine RANKL prote
5	1675	100.0	316 21	AAW91024 Mouse OBM protein
6	1675	100.0	316 21	AAW84418 Amino acid sequenc
7	1675	100.0	316 21	AAW84419 Amino acid sequenc
8	1675	100.0	316 23	AAW78289 Mouse TRANCE prote
9	1597	95.3	318 22	AAW82092 Rat osteoclast dif
10	1554	92.8	294 19	AAW69956 NF-kB receptor act

11	1554	92.8	294	19	AAW68292	NF-kB receptor act
12	1554	92.8	294	22	AAE08737	Murine receptor ac
13	1554	92.8	294	22	AAE04425	Murine receptor ac
14	1554	92.8	294	22	AAE01992	Murine RANKL (rece
15	1417.5	84.6	317	19	AAW83195	Human osteoprotege
16	1417.5	84.6	317	19	AAW69957	NF-kB receptor act
17	1417.5	84.6	317	19	AAW68293	NF-kB receptor act
18	1417.5	84.6	317	21	AAW84417	Amino acid sequenc
19	1417.5	84.6	317	22	AAE08738	Human receptor act
20	1417.5	84.6	317	22	AAE04426	Human full-length
21	1417.5	84.6	317	22	AAE01993	Human RANKL polye
22	1417.5	84.6	317	23	ABW08134	Human TRANCE prote
23	1417.5	84.6	317	23	AAU78285	Osteoclastogenesis
24	1409.5	84.1	317	19	AAW83018	Amino acid sequenc
25	1318	78.7	501	22	AAW84420	A murine OCIF-bind
26	1297	77.4	244	19	AAW83019	Osteoclastogenesis
27	1107	66.1	246	19	AAW83020	Human TRANCE. Hom
28	1101	65.7	245	20	AAW17873	Human PRO206 polyp
29	1100	65.7	244	23	AAU78286	Human TRANCE prote
30	1100	63.7	244	23	AAU78286	GlutathioneStransf
31	960	57.3	409	23	AAO17115	Murine GST-modf fu
32	960	57.3	409	23	AAW49711	Amino acid sequenc
33	855	51.0	160	21	AAE08272	Amino acid sequenc
34	852	50.9	173	21	AAW84421	Amino acid sequenc
35	852	50.9	187	21	AAW84420	A murine osteoprot
36	842	50.3	173	21	AAW84422	Mouse FLAG-murine
37	830	49.6	170	22	AAU08386	An osteoprotegerin
38	804.5	48.0	188	21	AAW84423	An osteoprotegerin
39	794.5	47.4	182	21	AAW84424	DNA encoding osteo
40	771	46.0	173	21	AAW84425	Amino acid sequenc
41	768	45.9	160	21	AAE08273	Mouse OBM protein
42	746	44.5	139	21	AAW91023	Human RANKL. Homo
43	741	44.2	152	22	AAW67248	An osteoprotegerin
44	732	43.7	173	21	AAW84426	Mouse OBM protein
45	387	23.1	74	21	AAW91020	

ALIGNMENTS

RESULT 1

AAW83194
ID AAW83194 standard; Protein: 316 AA.

XX AC AAW83194;

XX DT 11-FEB-1999 (first entry)

XX DE Human osteoprotegerin binding protein from the 32D-F3 ins.

XX DE Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
hypercalcaemia; osteoclast differentiation and activation receptor;
Paget's disease.

XX OS Homo sapiens.

XX PN WO9846751-A1.

XX PD 22-OCT-1998.

XX PF 15-APR-1998; 98WO-US07584.

XX PR 30-MAR-1998; 98US-0052521.

XX PR 16-APR-1997; 97US-0842842.

XX PR 23-JUN-1997; 97US-0880855.

XX PA (AMGE-) AMGEN INC.

XX FI Boyle WJ;

XX DR WPI; 1998-594578/50.

XX DR N-PSDB; AAW70284.

XX Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis
 XX
 PS Claim 19; Fig 1; 47pp; English.
 XX
 CC The present sequence is human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OC) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 XX
 SQ Sequence 316 AA;
 Query Match 100.0%; Score 1675; DB 19; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-143;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRASRDYGYLRSSEMGSGCPVHEGLHPAPAPAPPPAASRSMFLALLGLGLGQ 60
 DB 1 MRRASRDYGYLRSSEMGSGCPVHEGLHPAPAPAPPPAASRSMFLALLGLGLGQ 60
 QY 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHFNAGLQDSTLESDTLPDCRRMKQ 120
 DB 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHFNAGLQDSTLESDTLPDCRRMKQ 120
 QY 121 AFQAVQKELQHVGPQFSGAPAMMEGSLDVAQKGPAPFAHLTINAASIPSGSHK 180
 DB 121 AFQAVQKELQHVGPQFSGAPAMMEGSLDVAQKGPAPFAHLTINAASIPSGSHK 180
 QY 181 VTLSSTYHWRGWAQKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYLQMWY 240
 DB 181 VTLSSTYHWRGWAQKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYLQMWY 240
 QY 241 VVTSIKIPSSHNLKMGSGTKNWSGSEPHFYISYNGVGFKLKAGEISIQVSNPSLLDP 300
 DB 241 VVTSIKIPSSHNLKMGSGTKNWSGSEPHFYISYNGVGFKLKAGEISIQVSNPSLLDP 300
 QY 301 DDATYFGAFKQVQDID 316
 DB 301 DDATYFGAFKQVQDID 316
 RESULT 2
 AA#83017
 ID AA#83017 standard; Protein; 316 AA.
 XX
 AC AA#83017;
 XX
 DT 10-FEB-1999 (first entry)
 XX
 DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
 XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism.
 XX
 OS Unidentified.
 XX

PN WO9846644-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-JP01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nagagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 XX
 DR WPI; 1998-594563/50.
 DR N-PSDB; AAV69886.
 XX
 PT Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 XX
 PS Claim 8; Pages 106-108; 151pp; Japanese.
 XX
 CC The present sequence represents an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 XX
 SQ Sequence 316 AA;
 Query Match 100.0%; Score 1675; DB 19; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-143;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRASRDYGYLRSSEMGSGCPVHEGLHPAPAPAPPPAASRSMFLALLGLGLGQ 60
 DB 1 MRRASRDYGYLRSSEMGSGCPVHEGLHPAPAPAPPPAASRSMFLALLGLGLGQ 60
 QY 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHFNAGLQDSTLESDTLPDCRRMKQ 120
 DB 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHFNAGLQDSTLESDTLPDCRRMKQ 120
 QY 121 AFQAVQKELQHVGPQFSGAPAMMEGSLDVAQKGPAPFAHLTINAASIPSGSHK 180
 DB 121 AFQAVQKELQHVGPQFSGAPAMMEGSLDVAQKGPAPFAHLTINAASIPSGSHK 180
 QY 181 VTLSSTYHWRGWAQKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYLQMWY 240
 DB 181 VTLSSTYHWRGWAQKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYLQMWY 240
 QY 241 VVTSIKIPSSHNLKMGSGTKNWSGSEPHFYISYNGVGFKLKAGEISIQVSNPSLLDP 300
 DB 241 VVTSIKIPSSHNLKMGSGTKNWSGSEPHFYISYNGVGFKLKAGEISIQVSNPSLLDP 300
 QY 301 DDATYFGAFKQVQDID 316
 DB 301 DDATYFGAFKQVQDID 316

RESULT 3

AAW59654
 ID AAW59654 standard; Protein; 316 AA.
 XX
 AC AAW59654;
 XX
 DT 24-SEP-1998 (first entry)
 XX
 DE Amino acid sequence of mouse 499E9 protein.
 XX
 KW Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
 KW antagonist; autoimmune disorder; rheumatoid arthritis;
 KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
 KW acute inflammatory response; antibody; antigen; cancer.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 Domain 1..49
 T /note= "intracellular domain"
 FT 70..316
 FT /note= "extracellular domain"
 XX
 PN W09825958-A2.
 XX
 PD 18-JUN-1998.
 XX
 PD 12-DEC-1997; 97WO-US22766.
 XX
 PR 13-DEC-1996; 96US-0032846.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Gorman DM, Mattson JD;
 XX
 DR WPI; 1998-348452/30.
 DR N-PSDB; AAV41489.
 XX
 PT Mouse cell surface antigen, 499E9 protein - used to treat conditions
 PT associated with abnormal physiology or development
 XX
 PS Claim 1; Pages 8-11; 59pp; English.
 XX
 CC This is the amino acid sequence of the mouse 499E9 protein, used
 CC in the method of the invention to treat conditions associated with
 CC abnormal physiology or development. The 499E9 protein is expressed
 CC highly on polarised Th1 T cells. Binding of 499E9 to its receptor may
 CC result in either immune cell expansion or apoptosis. Antagonists of
 CC 499E9 may be used to modulate immune responses in abnormal situations,
 CC e.g. autoimmune disorders including rheumatoid arthritis, systemic
 CC lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
 CC acute inflammatory responses in which T-cell expansion, activation or
 CC immunological T-cell memory play an important role. The antibodies
 CC can be used to raise anti-idiotypic antibodies which will be useful
 CC in detecting or diagnosing various immunological conditions related to
 CC the expression of antigens of 499E9. The antibodies, and fragments of
 CC 499E9 can be used in the treatment of conditions associated with
 CC abnormal physiology or development, including abnormal proliferation
 CC (e.g. cancerous conditions) or degenerative conditions.
 XX
 SQ Sequence 316 AA;
 Query Match 100.0%; Score 1675; DB 19; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-143;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRASRDYGYLRSEEMSGGPGVPHGGLHPAPSAFAPAPPPAASRSMFLALGLGLGQ 60
 DB 1 MRRASRDYGYLRSEEMSGGPGVPHGGLHPAPSAFAPAPPPAASRSMFLALGLGLGQ 60
 QY 61 VVCSTALFLFRAQMDPNRISDTHCFYRLRLHFNAGLQDSTLESDTLPDCRRMKQ 120
 DB 61 VVCSTALFLFRAQMDPNRISDTHCFYRLRLHFNAGLQDSTLESDTLPDCRRMKQ 120

QY 121 AFOGAVOKELQHVGPQRFSGAPAMEGSWLDVAQRGKPEAQFPAHLTINAASIPSGSHK 180
 DB 121 AFOGAVOKELQHVGPQRFSGAPAMEGSWLDVAQRGKPEAQFPAHLTINAASIPSGSHK 180
 QY 181 VTLSSTWYHGRGAKISNMTLSNCKLRVNDGFYLLVANICFRHHETSGSVPTDYLOLMVY 240
 DB 181 VTLSSTWYHGRGAKISNMTLSNCKLRVNDGFYLLVANICFRHHETSGSVPTDYLOLMVY 240
 QY 241 VKVTSIKIPSSHNLKMGSGTKNSGSEHFYSINVGGFKLAGEEISIQVSNPSSLDP 300
 DB 241 VKVTSIKIPSSHNLKMGSGTKNSGSEHFYSINVGGFKLAGEEISIQVSNPSSLDP 300
 QY 301 DQDATYFGAFKVDID 316
 DB 301 DQDATYFGAFKVDID 316
 RESULT 4
 AAY17874
 ID AAY17874 standard; Protein; 316 AA.
 XX
 AC AAY17874;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Murine TRANCE.
 XX
 KW TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
 KW TNF-related activation induced cytokine; immune response; cancer;
 KW autoimmune disease; HIV; hypersensitivity; allergen.
 XX
 OS Mus musculus.
 XX
 PN W09929865-A2.
 XX
 PD 17-JUN-1999.
 XX
 PD 14-DEC-1998; 98WO-US26486.
 XX
 PR 11-DEC-1998; 98US-0989479.
 PR 12-DEC-1997; 97US-0989479.
 PR 03-MAR-1998; 98US-0034099.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Choi Y, Josien R, Steinman R, Won B;
 XX
 DR WPI; 1999-385609/32.
 DR N-PSDB; AAX80224.
 XX
 PT TNF like proteins for treating autoimmunity and cancer
 XX
 PS Claim 9; Fig 3; 164pp; English.
 CC
 CC The present sequence represents murine TNF-related activation induced
 CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their
 CC variants, fragments, derivatives or analogues may be used as modulators
 CC of immune response in a mammal comprising, antisense sequences to
 CC TRANCE and fusion proteins comprising human and/or murine TRANCE.
 CC Agonists and antagonists of TRANCE, can be used to modulate immune
 CC response by increasing or decreasing the life span of mature dendritic
 CC cells and increasing or decreasing T cell activation. These techniques
 CC are especially useful for treating immune system related conditions such
 CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
 CC The TRANCE polypeptides can be used to increase the viability of
 CC dendritic cells in vivo or in vitro, especially when used in conjunction
 CC with proteins of the tumour necrosis factor (TNF) superfamily (especially
 CC CD40L or TNF-alpha).
 XX
 SQ Sequence 316 AA;
 Query Match 100.0%; Score 1675; DB 20; Length 316;

Best Local Similarity 100.0%; Pred. No. 2.6e-143; Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYKYLRSSEEMSGPGVPEHPLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
 DB 1 MRRASRDYKYLRSSEEMSGPGVPEHPLPAPSAPAPPPAASRSMFLALLGLGLGQ 60

QY 61 VVCSIALFLYFRAQMDPNRISSESTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120
 DB 61 VVCSIALFLYFRAQMDPNRISSESTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120

QY 121 AFOGAVOKELQIHVGPQRFSGAPAMMEGSLDVAQRGPEAPFAHLTINAAISIPSGSHK 180
 DB 121 AFOGAVOKELQIHVGPQRFSGAPAMMEGSLDVAQRGPEAPFAHLTINAAISIPSGSHK 180

QY 181 VTLSSWYHDSRWAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLQVMY 240
 DB 181 VTLSSWYHDSRWAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLQVMY 240

QY 241 VVTSIKIPSSHNLMKGGSTKNWNSGFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300
 DB 241 VVTSIKIPSSHNLMKGGSTKNWNSGFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300

QY 301 DQDATYFGAFKQVQDID 316
 DB 301 DQDATYFGAFKQVQDID 316

RESULT 5
 ID AAY91024 standard; Protein: 316 AA.
 AC AAY91024;
 DT 05-SEP-2000 (first entry)
 DE Mouse OBM protein sequence SEQ ID NO:10.
 KW Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF;
 KW OBM; osteoclast; bone absorption promoting factor; vitamin D3; PTH;
 KW parathyroid hormone.
 OS Mus sp.
 PN JP2000102390-A.
 PD 11-APR-2000.
 PF 30-SEP-1998; 98JP-0292971.
 PS 30-SEP-1998; 98JP-0292971.
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 PA (YSNE-) YS NEW TECHNOLOGY KENYUSHO.
 DR WPI; 2000-332087/29.
 DR N-PSDB; AAA39156.
 PT A DNA and preparation of a protein by using it
 PS Example 1; Page 15-16; 18pp; Japanese.
 CC The present invention describes a genomic DNA encoding a protein having an activity of supporting or promoting differentiation and maturation of osteoclasts. The genomic DNA encoding a protein has the following properties: (a) combines specifically with osteoclastogenesis inhibitory factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw) of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide gel electrophoresis) under a nonreductive condition and the apparent mw when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c) has an activity of supporting or promoting differentiation and maturation of osteoclast in the co-culture of mouse osteoblast-like stroma cell and mouse spleen cell in the presence of a bone absorption promoting factor

CC such as active type vitamin D3 and parathyroid hormone (PTH). The protein can be used as a drug and a research reagent. The present sequence represents a mouse OCIF binding molecule (OBM) from the present invention.

QY 1 MRRASRDYKYLRSSEEMSGPGVPEHPLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
 DB 1 MRRASRDYKYLRSSEEMSGPGVPEHPLPAPSAPAPPPAASRSMFLALLGLGLGQ 60

QY 61 VVCSIALFLYFRAQMDPNRISSESTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120
 DB 61 VVCSIALFLYFRAQMDPNRISSESTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120

QY 121 AFOGAVOKELQIHVGPQRFSGAPAMMEGSLDVAQRGPEAPFAHLTINAAISIPSGSHK 180
 DB 121 AFOGAVOKELQIHVGPQRFSGAPAMMEGSLDVAQRGPEAPFAHLTINAAISIPSGSHK 180

QY 181 VTLSSWYHDSRWAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLQVMY 240
 DB 181 VTLSSWYHDSRWAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLQVMY 240

QY 241 VVTSIKIPSSHNLMKGGSTKNWNSGFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300
 DB 241 VVTSIKIPSSHNLMKGGSTKNWNSGFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300

QY 301 DQDATYFGAFKQVQDID 316
 DB 301 DQDATYFGAFKQVQDID 316

RESULT 6
 ID AAY84418 standard; Protein: 316 AA.
 AC AAY84418;
 DT 25-JUL-2000 (first entry)
 DE Amino acid sequence of a murine osteoprotegerin ligand (OPGL).
 KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KW tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator;
 KW immune response; osteoporosis; bone resorption.
 OS Mus musculus.
 FH Key - Location/Qualifiers
 FT Domain 48..71 /note= "transmembrane domain"
 FT Domain 70..157 /note= "extracellular stalk domain"
 FT Domain 152..316 /note= "tumour necrosis factor-like domain"
 FT Region 158..317 /note= "active ligand moiety"
 PN WO200015807-A1.
 PD 23-MAR-2000.
 PF 13-SEP-1999; 99WO-DK00481.
 PR 15-SEP-1998; 98DK-0001164.
 PR 02-OCT-1998; 98US-0102896.
 PA (MEBI-) M & E BIOTECH AS.

XX PI Halkier T, Haaning J;
 XX FT WPI: 2000-271444/23.
 DR DR N-PSDB; AAZ99965.
 XX XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 PT PT to treat, prevent and ameliorate osteoporosis -
 XX XX Claim 17; Page 81-82; 110pp; English.
 XX XX The present sequence represents a murine osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.
 XX XX Sequence 316 AA;
 Query Match 100.0%; Score 1675; DB 21; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-143;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRASRDYKYLRSSEMGSGVPHEGPHLPAPSAPAPAPPPAASRSNMFALLGLGLGQ 60
 Db 1 MRRASRDYKYLRSSEMGSGVPHEGPHLPAPSAPAPAPPPAASRSNMFALLGLGLGQ 60
 QY 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLESDTLPDSCRMKQ 120
 Db 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLESDTLPDSCRMKQ 120
 QY 121 AFOGAVQKELQHVGPQFSGAPAMEGSWLDVAQGRKPEAOPFAHLITNAASIPSGSHK 180
 Db 121 AFOGAVQKELQHVGPQFSGAPAMEGSWLDVAQGRKPEAOPFAHLITNAASIPSGSHK 180
 QY 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLVMY 240
 Db 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLVMY 240
 QY 301 DDATYFGAFKVDID 316
 Db 301 DDATYFGAFKVDID 316
 RESULT 7
 ID AA84419 standard; Protein; 316 AA.
 XX AC AA84419;
 XX DT 25-JUL-2000 (first entry)
 XX DE Amino acid sequence of a murine osteoprotegerin ligand (OPGL).
 XX KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KW tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator;
 KW immune response; osteoporosis; bone resorption.
 XX OS Mus musculus.

XX FH Key Location/Qualifiers
 FT Region 49..69
 FT Domain /note= "transmembrane region"
 FT Domain 70..157
 FT Region /note= "extracellular stalk domain"
 FT Region 158..317
 FT Region /note= "active ligand moiety"
 XX PN WO200015807-A1.
 XX XX 23-MAR-2000;
 XX XX 13-SEP-1999; 99WO-DK00481.
 XX XX 15-SEP-1998; 98DK-0001164.
 PR 02-OCT-1998; 98US-0102896.
 XX (MEBI-) M & E BIOTECH AS.
 XX Halkier T, Haaning J;
 WPI: 2000-271444/23.
 DR N-PSDB; AAZ99966.
 XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 PT PT to treat, prevent and ameliorate osteoporosis -
 XX XX Claim 17; Page 85-86; 110pp; English.
 CC The present sequence represents a murine osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.
 XX XX Sequence 316 AA;
 Query Match 100.0%; Score 1675; DB 21; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-143;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRASRDYKYLRSSEMGSGVPHEGPHLPAPSAPAPPPAASRSNMFALLGLGLGQ 60
 Db 1 MRRASRDYKYLRSSEMGSGVPHEGPHLPAPSAPAPPPAASRSNMFALLGLGLGQ 60
 QY 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLESDTLPDSCRMKQ 120
 Db 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLESDTLPDSCRMKQ 120
 QY 121 AFOGAVQKELQHVGPQFSGAPAMEGSWLDVAQGRKPEAOPFAHLITNAASIPSGSHK 180
 Db 121 AFOGAVQKELQHVGPQFSGAPAMEGSWLDVAQGRKPEAOPFAHLITNAASIPSGSHK 180
 QY 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLVMY 240
 Db 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLVMY 240
 QY 241 VKTSIKIPSSHNLMKGGSTKNWNSGSEPHFYSINVGGFFKLAGEEISIQVNSPLDLP 300
 Db 241 VKTSIKIPSSHNLMKGGSTKNWNSGSEPHFYSINVGGFFKLAGEEISIQVNSPLDLP 300
 QY 301 DDATYFGAFKVDID 316
 Db 301 DDATYFGAFKVDID 316

Db 301 DQDATYFGAFKVDID 316

RESULT 8
AAU78289
ID AAU78289 standard; Protein; 316 AA.

XX
AC AAU78289;
XX
DT 18-JUN-2002 (first entry)
XX
DE Mouse TRANCE protein.
XX
KW Mouse; tumour necrosis factor-related activation induced cytokine;
KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;
KW rheumatoid arthritis; acromegaly; gigantism; exostosis; carilagines;
KW exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
KW cartilage growth; skeletal growth.
XX
QS Mus sp.
WO200216551-A2.
XX
PD 28-FEB-2002.
XX
PF 20-AUG-2001; 2001WO-US26101.
XX
PR 18-AUG-2000; 2000US-226197P.
XX
PA (UTWA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX
PI Choi Y, Odgren PR, Marks SC;
XX
DR WPI; 2002-304119/34.
XX
DR N-PSDB; ABK12880.
XX
PT Treating mammal having disorder characterised by abnormal
PT cartilage/skeletal growth such as dwarfism, acromegaly, by
PT administering tumour necrosis factor-related activation induced
PT cytokine-modulating agent to mammal -
XX
PS Disclosure; Fig 10; 55pp; English.
XX
CC The present invention relates to a new method of treating a mammal
CC having a disorder comprising insufficient or excessive cartilage or
CC skeletal growth. The method of the invention involves administering to
CC the mammal a tumour necrosis factor-related activation induced cytokine
CC (TRANCE)-modulating agent. The method is useful for treating a mammal
CC having a disorder comprising insufficient or excessive cartilage or
CC skeletal growth, where the disorder comprising insufficient cartilage or
CC or skeletal growth is selected from dwarfism, osteopetrosis,
CC craniofacial-skeletal discrepancies and bone or cartilage damage
CC resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
CC arthritis, and disorders comprising excessive cartilage or skeletal
CC growth are selected from acromegaly, gigantism, exostosis, carilagines,
CC exostosis bursata and multiple osteocartilaginous exostoses. The method
CC is useful for inhibiting chondrocyte differentiation. The present
CC amino acid sequence represents the mouse TRANCE protein of the invention.
CC TRANCE is a member of the tumour necrosis factor family and acts
CC directly on cartilage-producing cells (chondrocytes).
XX
SQ Sequence 316 AA;
Query Match 100.0%; Score 1675; DB 23; Length 316;
Best Local Similarity 100.0%; Pred. No. 2-6e-143;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYKYLRSSEMGSGVPEHGLHPAPAPAPPPAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYKYLRSSEMGSGVPEHGLHPAPAPAPPPAASRSMFLALLGLGLGQ 60
QY 61 VVCSIALFLYFRAQMDPNRISSESTHCFYRIILRLHENAGLQDSTLESEDTLPDSCRMMQ 120

Db 61 VVCSIALFLYFRAQMDPNRISSESTHCFYRIILRLHENAGLQDSTLESEDTLPDSCRMMQ 120
QY 121 AFOGAVOKELQHVGPQFSGAPAMMEGSLDVAQGRPEAOPFAHLTINAASIPSGSHK 180
Db 121 AFOGAVOKELQHVGPQFSGAPAMMEGSLDVAQGRPEAOPFAHLTINAASIPSGSHK 180
QY 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNODGFFYYLYANICFRHHETSGSVPTDYDLQMY 240
Db 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNODGFFYYLYANICFRHHETSGSVPTDYDLQMY 240
QY 241 VVTKSIKIPSSHNLMKGGSTKNWNSSEPHYSINVGPFKLRAGEISIOVSNPSLLDP 300
Db 241 VVTKSIKIPSSHNLMKGGSTKNWNSSEPHYSINVGPFKLRAGEISIOVSNPSLLDP 300
QY 301 DQDATYFGAFKVDID 316
Db 301 DQDATYFGAFKVDID 316

RESULT 9
AAB82092
ID AAB82092 standard; Protein; 318 AA.
XX
AC AAB82092;
XX
DT 29-JUN-2001 (first entry)
XX
DE Rat osteoclast differentiation factor, ODF.
XX
KW Rat; osteoclast formation inducer; vaccine; gene therapy;
KW Osteoclast Differentiation Factor; bone.
XX
OS Rattus sp.
XX
PN WO200123549-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-AU01202.
XX
PR 29-SEP-1999; 99AU-0003147.
XX
PA (UTWA-) UNIV WESTERN AUSTRALIA.
XX
PI Xu J, Zheng M;
XX
DR WPI; 2001-335526/35.
XX
DR N-PSDB; AAF86481.
XX
PT Novel nucleic acid encoding rat osteoclast differentiation factor
PT useful for modulating activity of a cell, e.g., cell proliferation,
PT cell differentiation and cell viability
XX
PS Claim 5; Fig 2; 81pp; English.
XX
CC The present sequence is the protein sequence for rat Osteoclast
CC Differentiation Factor (ODF). ODF is thought to be directly involved in
CC the differentiation of monocytes/macrophages into osteoclasts.
CC Osteoclasts promote dissolution of the bone matrix and solubilisation of
CC bone salts. The ODF coding sequence is useful in gene therapy, and as
CC hybridisation probes or primers. ODF protein is useful for modulating the
CC activity of cells, e.g., cell proliferation, cell differentiation and
CC cell viability, as immunogens to generate anti-rat ODF antibodies, and
CC as vaccines. Anti-rat ODF antibodies are useful in assay methods for
CC quantifying ODF polypeptides.
XX
SQ Sequence 318 AA;
Query Match 95.3%; Score 1597; DB 22; Length 318;
Best Local Similarity 95.0%; Pred. No. 3e-136;
Matches 302; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 MRRASRDYGYKLSSEMGSGPGVHEGPHLPAPAPAPAPPPAASRSMFLALGLGLGQ 60
 DB 1 MRRANRDYGYKLSSEMGSGPGVHEGPHLPAPAPAPAPPPAASRSMFLALGLGLGQ 60
 QY 61 VVCSIALFLYFRAQMDPNRISSESTHCFYRILRLHENAGLQDSTLESDT--LPDSCRRM 118
 DB 61 VVCSIALFLYFRAQMDPNRISSESTHCFYRILRLHENAGLQDSTLESDT--LPDSCRRM 120
 QY 119 KQAFQAVQKELQHVGPQRFSGPAPAMEGSWLDVAQKPEAQPFAHLTINAAIPSGS 178
 DB 121 KQAFQAVQKELQHVGPQRFSGPAPAMEGSWLDVAQKPEAQPFAHLTINAAIPSGS 180
 QY 179 HKVTLSSWYHNRGWAKISNMTLSNGKLRVNDGFYILYANICFRHHETSGSVPTDYQLM 238
 DB 181 HKVTLSSWYHNRGWAKISNMTLSNGKLRVNDGFYILYANICFRHHETSGSVPTDYQLM 240
 QY 239 VYVYKTSIKIPSSHNLMKGGSTKNWNSGSEHFYSINVGFFKLRAGEEISIQVSNPSSL 298
 DB 241 VYVYKTSIKIPSSHNLMKGGSTKNWNSGSEHFYSINVGFFKLRAGEEISIQVSNPSSL 300
 QY 299 DPQDATYFGAFKVQDID 316
 DB 301 DPQDATYFGAFKVQDID 318

RESULT 10

AAW69956
 ID AAW69956 standard; Protein: 294 AA.

XX AC AAW69956;

XX DT 08-OCT-1998 (first entry)

XX DE NF-kB receptor activator RANK ligand (RANKL).

XX KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 XX KW immune response; inflammatory response; toxic shock; sepsis;
 XX KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.

XX OS Mus musculus.

XX PN WO9828426-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23775.

XX PR 14-OCT-1997; 97US-0064671.

XX PR 23-DEC-1996; 96US-0059978.

XX PR 07-MAR-1997; 97US-0813509.

XX PA (IMMUNEX CORP.

XX PI Anderson DM, Galibert LJ, Maraskovsky E;

XX XX WPI; 1998-377657/32.

XX DR N-PSDB; AAV41377.

XX XX New isolated ligand for receptor activator of NF-kappa B - used to

XX XX develop products for augmenting an immune response for inhibiting an

XX XX inflammatory response and for protection of cells

XX XX Claim 27; Pages 55-57; 80pp; English.

XX XX This represents a murine RANKL, a ligand for the RANK (receptor

XX XX activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a

XX XX member of the tumour necrosis factor (TNF) family. A soluble RANK

XX XX may be used for inhibiting activation of NF-kB, by contacting a cell

XX XX expressing membrane-associated RANK with a soluble RANK which binds to

CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
 CC may be useful in ameliorating negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
 CC reactions. They can also be used in adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides
 CC can also be used to identify inhibitors of RANK and thus inhibitors of
 CC an inflammatory response, and also for protecting RANK-expressing cells
 CC from the negative effects of chemotherapy or the presence of high levels
 CC of TNF-alpha. The products can also be used for detection and drug
 CC screening.

XX SQ Sequence 294 AA;

Query Match 92.88; Score 1554; DB 19; Length 294;

Best Local Similarity 99.7%; Pred. No. 2.1e-132;

Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGPHLPAPAPAPPPAASRSMFLALGLGLGQVCSIALFLYFRAQMDPNRISE 82

DB 1 GVPHEGPHLPAPAPAPPPAASRSMFLALGLGLGQVCSIALFLYFRAQMDPNRISE 60

QY 83 DSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKAQFQAVQKELQHVGPQRFSGA 142

DB 61 DSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKAQFQAVQKELQHVGPQRFSGA 120

QY 143 PAMMEGSWLDVAQKPEAQPFAHLTINAAIPSGSHKVTLSWYHNRGWAKISNMTLSN 202

DB 121 PAMMEGSWLDVAQKPEAQPFAHLTINAAIPSGSHKVTLSWYHNRGWAKISNMTLSN 180

QY 203 GKLRVNDGFYILYANICFRHHETSGSVPTDYQLMVTWVTKSIKIPSSHNLMKGGSTKN 262

DB 181 GKLRVNDGFYILYANICFRHHETSGSVPTDYQLMVTWVTKSIKIPSSHNLMKGGSTKN 240

QY 263 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSSLDPQDATYFGAFKVQDID 316

DB 241 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSSLDPQDATYFGAFKVQDID 294

RESULT 11

AAW68292

ID AAW68292 standard; Protein: 294 AA.

XX AC AAW68292;

XX DT 08-OCT-1998 (first entry)

XX DE NF-kB receptor activator RANK ligand (RANKL).

XX KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 XX KW immune response; inflammatory response; toxic shock; sepsis;
 XX KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.

XX OS Mus musculus.

XX PN WO9828424-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23866.

XX PR 14-OCT-1997; 97US-0064671.

XX PR 23-DEC-1996; 96US-0059978.

XX PR 07-MAR-1997; 97US-0813509.

XX PA (IMMUNEX CORP.

XX PI Anderson DM, Galibert LJ, Maraskovsky E;

XX XX WPI; 1998-377655/32.

XX DR N-PSDB; AAV41371.

XX XX New isolated receptor activator of necrosis factor-kappa B - useful

PT for, e.g. developing products for regulating an immune or
 PT inflammatory response, treating toxic shock or sepsis
 PS
 PS Example 7; Pages 55-57; 80pp; English.

XX This represents a murine RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
 CC member of the tumor necrosis factor (TNF) family. Host cells transfected
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX Sequence 294 AA;

Query Match 92.8%; Score 1554; DB 19; Length 294;
 Best Local Similarity 99.7%; Pred. No. 2.1e-132;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGLHPAPSAPAPPPAASRSMFLALLGLGLGVGVCSIALFLYFRQMDPNRISE 82
 DB 1 GVPHEGLHPAPSAPAPPPAASRSMFLALLGLGLGVGVCSIALFLYFRQMDPNRISE 60
 QY 83 DSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQAFQAVOKELQHVGPORFSGA 142
 DB 61 DSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQAFQAVOKELQHVGPORFSGA 120
 QY 143 PAMEGSWLDVAQRGKPEAQPFALHTINAASIPSGSHKVTLSSTHWRGAKISNMTLSN 202
 DB 121 PAMEGSWLDVAQRGKPEAQPFALHTINAASIPSGSHKVTLSSTHWRGAKISNMTLSN 180
 QY 203 GKLRVNDGFYLYANICFRHETSGSVPTDYQLQMVVTVKTSIKIPSSHNLKMGSTKN 262
 DB 181 GKLRVNDGFYLYANICFRHETSGSVPTDYQLQMVVTVKTSIKIPSSHNLKMGSTKN 240
 QY 263 WSGNSEFHYISINVGFFKLRAGEISIQVSNPSLLDDPDQDATYFGAFKVQDID 316
 DB 241 WSGNSEFHYISINVGFFKLRAGEISIQVSNPSLLDDPDQDATYFGAFKVQDID 294

RESULT 12

AAE08737 AAE08737 standard; Protein; 294 AA.

AAE08737;

15-NOV-2001 (first entry)

DE Murine receptor activator of NF kappaB ligand (RANKL) protein.

XX Murine; receptor activator of nuclear factor kappaB ligand; RANKL; NF;
 KW tumor necrosis factor; TNF; TNF receptor associated factor; TRAF;
 KW immune response; inflammatory response; graft-versus-host reaction;
 KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
 KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

OS Mus musculus.

XX US6271349-B1.

XX 07-AUG-2001.

XX 17-DEC-1998; 9805-0215649.

XX 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0077181.
 PR 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0772330.
 PR 07-MAR-1997; 97US-0813509.
 PR 22-DEC-1997; 97US-0996139.
 XX (TMV) IMMUNEX CORP.

PA Dougall WC, Galibert L;

PI WPI; 2001-520313/57.

DR N-PSDB; AAD15310.

XX New receptor activator of NF-kappaB (RANK) polypeptides, useful for
 PT regulating immune response, in screening for RANK inhibitors, or as an
 PT adjunct therapy for disease characterized by neoplastic cells that
 PT express RANK

XX Example 15; Column 65-68; 47pp; English.

CC The patent discloses novel receptor activator of nuclear factor (NF)-
 CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member
 CC of the tumor necrosis factor (TNF) receptor superfamily and associates
 CC with TNF receptor associated factor (TRAF) 2 and 3 which are important
 CC in the regulation of immune and inflammatory response. The receptors
 CC are useful for regulating immune response and in screening for inhibitors
 CC of these receptors. The cytoplasmic domain of RANK is used in developing
 CC assays for inhibitors of signal transduction, e.g. for screening the
 CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
 CC TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists
 CC are useful in ameliorating the negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, acute inflammatory
 CC reactions and the effects of bone resorption. RANK acts as an anti-
 CC apoptotic signal and rescue the cells that express RANK from apoptosis.
 CC Soluble forms of the receptor are used in vivo or in vitro based
 CC screening tests for agonists or antagonists of RANK activity, as
 CC antagonists of RANK-mediated NF-kappa B activation, or to inhibit
 CC transduction of a signal via RANK. RANK compositions are used in the
 CC development of both agonistic and antagonistic antibodies, or as an
 CC adjunct therapy for disease characterised by neoplastic cells that
 CC express RANK. Compounds that interfere with RANK/TRAF6 interactions
 CC are useful for modulating the formation of osteoclasts from osteoclast
 CC precursors and for modulating osteoclast function and activities. They
 CC are used as inhibitors of diseases associated with excess bone resorption
 CC and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are
 CC useful for the expression of recombinant proteins, as probes for analysis
 CC of the presence or distribution of RANK transcripts, while the proteins
 CC are useful in preparing kits for the detection of soluble RANK, or
 CC monitor RANK-related activity. The present sequence is RANK ligand
 CC (RANKL) protein from murine.

XX SQ Sequence 294 AA;

Query Match 92.8%; Score 1554; DB 22; Length 294;

Best Local Similarity 99.7%; Pred. No. 2.1e-132;

Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGLHPAPSAPAPPPAASRSMFLALLGLGLGVGVCSIALFLYFRQMDPNRISE 82

DB 1 GVPHEGLHPAPSAPAPPPAASRSMFLALLGLGLGVGVCSIALFLYFRQMDPNRISE 60

QY 83 DSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQAFQAVOKELQHVGPORFSGA 142

DB 61 DSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQAFQAVOKELQHVGPORFSGA 120

QY 143 PAMEGSWLDVAQRGKPEAQPFALHTINAASIPSGSHKVTLSSTHWRGAKISNMTLSN 202

DB 121 PAMEGSWLDVAQRGKPEAQPFALHTINAASIPSGSHKVTLSSTHWRGAKISNMTLSN 180

QY 203 GKLRVNDGFYLYANICFRHETSGSVPTDYQLQMVVTVKTSIKIPSSHNLKMGSTKN 262

DB 181 GKLRVNDGFYLYANICFRHETSGSVPTDYQLQMVVTVKTSIKIPSSHNLKMGSTKN 240

QY 263 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 316
 DB 241 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 294

RESULT 13

AAE04425
 ID AAE04425 standard; Protein; 294 AA.

XX AC AAE04425;

DT 04-SEP-2001 (first entry)

DE Murine receptor activator of NF- χ 1 B ligand (RANKL) protein.

KW Murine; receptor activator of NF- χ 1 B; RANK; tumour necrosis factor;
 W CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF;
 X chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.

OS Mus musculus.

PH Key Location/Qualifiers

FT Region 139..294

FT /note="Receptor binding region"

XX US6242213-B1.

XX 05-JUN-2001.

XX 22-DEC-1997; 97US-0995659.

XX 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0077181.

PR 14-OCT-1997; 97US-0064671.

XX (IMM V) IMMUNEX CORP.

XX Anderson DM;

XX WPI; 2001-407216/43.

DR N-PSDB; AAD08714.

XX New DNA molecules, useful for producing ligands (which are useful for
 PT regulating immune response and in screening for inhibitors of NF- χ 1 B
 PT receptor activator) of the receptor activator of NF- χ 1 B (RANK)

XX Example 7; Column 59-62; 43pp; English.

XX The present invention relates to receptor activator of NF- χ 1 B (RANK)
 CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
 CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
 CC proteins respectively. RANK is a member of the tumour necrosis factor
 CC (TNF) superfamily and it closely resembles CD40 in the extracellular
 CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
 CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
 CC The ligands are useful for regulating immune response and in screening
 CC for inhibitors of RANK. The present sequence is murine RANKL protein.

XX Sequence 294 AA;

Query Match 92.8%; Score 1554; DB 22; Length 294;

Best Local Similarity 99.7%; Pred. No. 2.1e-132;

Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGLHPAPSAPAPPPAASRSMFTALLGLGLGVVCSIALFLYFRAQMDPNRISE 82

DB 1 GVPHEGLHPAPSAPAPPPAASRSMFTALLGLGLGVVCSIALFLYFRAQMDPNRISE 60

QY 83 DSPHCFVRLRLHENAGLDSTLESDTLPSDCRRMKQAPQAVQKELQHVGPQPSGA 142

DB 61 DSTHCFVRLRLHENAGLDSTLESDTLPSDCRRMKQAPQAVQKELQHVGPQPSGA 120

QY 143 PAMMEGSLDVAORCKPEAQPFAHLTINAASIPSGSHKVTLSLSSWYHDRGWAKISNMTLSN 202
 DB 121 PAMMEGSLDVAORCKPEAQPFAHLTINAASIPSGSHKVTLSLSSWYHDRGWAKISNMTLSN 180
 QY 203 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLQMLVYVVKTSIKIPSSHNLKMGSGTKN 262
 DB 181 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLQMLVYVVKTSIKIPSSHNLKMGSGTKN 240
 QY 263 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 316
 DB 241 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 294

RESULT 14

AAE01992
 ID AAE01992 standard; Protein; 294 AA.

XX AC AAE01992;

DT 31-JUL-2001 (first entry)

DE Murine RANKL (receptor activator of NF- χ 1 B ligand) protein.

KW Mouse; receptor activator of NF- χ 1 B; RANK; nuclear factor- χ 1 B;
 KW NF- χ 1 B; tumour necrosis factor; TNF; type 1 transmembrane protein;
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KW immune system dysfunction; familial expansile osteolysis; FEO;
 KW early onset Paget's disease of bone; BP; cytostatic.

OS Mus musculus.

XX WO200136637-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-US31459.

XX 17-NOV-1999; 99US-0442029.

XX (IMM V) IMMUNEX CORP.

XX Anderson DM, Hughes AE;

XX WPI; 2001-329222/34.

DR N-PSDB; AAD05903.

XX New DNA encoding a receptor activator of NF- χ 1 B polypeptide for the
 PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
 PT Disclosure; Page 74-75; 96pp; English.

XX The present invention relates to a novel receptor, referred to as RANK

XX (receptor activator of NF (nuclear factor)- χ 1 B), a member of TNF
 CC (tumour necrosis factor) receptor superfamily. RANK is a type 1
 CC transmembrane protein that interacts with TNF receptor-associated
 CC factors (TRAFs). Triggering of RANK by overexpression or co-expression
 CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation
 CC of the transcription factor NF- χ 1 B, a ubiquitous transcription factor
 CC that is most extensively utilised in cells of the immune system.

XX Inhibition of NF- χ 1 B by RANK antagonists is useful in ameliorating
 CC negative effects of inflammatory reactions, and the effects of excess
 CC bone resorption. The RANK DNAs, proteins and their analogues are useful
 CC for the preparation of pharmaceutical compositions, for infecting target
 CC cells for use in gene therapy applications in diagnosing diseases
 CC associated with RANK, and as targets for use in screening assays. They
 CC may be used in the treatment or diagnosis of immune system dysfunction.
 CC The present invention also encompasses gene therapy methods to correct
 CC gene-activating mutations, associated with e.g. familial expansile
 CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
 CC present amino acid sequence is murine RANKL (murRANKL) protein.

XX Sequence 294 AA;

```

CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to osteoclast differentiation
CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of
CC OPG binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.
```

xx

```

SQ Sequence          317 AA;
Query Match           84.6%; Score 1417.5; DB 19; Length 317;
Best Local Similarity 84.3%; Pred. No. 5; Ae-120;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;
```

QY 1 MRRASDYKLYLRSSSEMGSGPVGHPGPHLPAPSAAPPAAASRMFLALGLGLQG 60
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 VVCSIALFLYFRAQMDPNRISEDSHTCFYRILRLHENAGLDSTPLESED - LPDCSRM 118
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 60 VVGSVALFFYFRAQMDPNRISEDSHTCIYRILRLHENADFQDTTLESQDKLIPDSCRRI 119
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 119 KQAFQGVQKELOHIYVQPFGSNGAPNMEGSLWDVAQRGPKEQPAHLTNINASIPSGS 178
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 120 KQAFQGVQKELOHIYVGSQHIRAEKANVDGSLWDLAKRSKLEAOPFAHLTINATIDPSGS 179
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 179 HKVTLSSTWYHDRGWAKISNTNLNGKLVRNQDFYYIYLANICFRHHETSGSVPTDYQLQM 238
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 180 HVSLSSTWYHDRGWAKISNTNFNGKLIVNQDFYYIYLANICFRHHETSGDLATEYLQLM 239
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 239 VYVTKYSIKTPSSHNLKMGGSTNWNSGNSEFHYSINVGGFFFKLRAGEEISIQVSNPSLL 298
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 240 VYVTKYSIKTPSSHNLKMGGSTKYWSGNSEFHYSINVGGFFFKLRSGEEISIEVSNPSLL 299
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 299 DPQDATIFGAFCVKQDID 316
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 300 DPQDATIFGAFCVKRDID 317

Search completed: April 16, 2003, 12:18:36
Job time : 34.5 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:17:02 ; Search time 15.5 Seconds
(without alignments)
1959.902 Million cell updates/sec

Title: US-09-787-126-6
Perfect score: 1675
Sequence: 1 MRRASRDYKYLRSSEMG.....LLDPDQATYFGAFKVDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185.5	11.1	261	2 S53090	CD40 ligand - bovi
2	183	10.9	278	2 A49266	fas ligand - rat
3	182	10.9	279	2 A53062	Fas ligand - mouse
4	173.5	10.4	281	2 I38707	Fas ligand - human
5	171.5	10.2	281	2 I53476	CD40 ligand - huma
6	157	9.4	260	2 S21738	CD40 ligand - mous
7	149	8.9	234	1 JQ1344	tumor necrosis fac
8	146.5	8.7	235	1 QWMSN	tumor necrosis fac
9	143.5	8.6	233	1 S22052	tumor necrosis fac
10	141	8.4	234	1 JH0529	tumor necrosis fac
11	140	8.4	233	2 S11688	tumor necrosis fac
12	139.5	8.3	233	1 QWUNH	tumor necrosis fac
13	137.5	8.2	234	1 A25451	tumor necrosis fac
14	135.5	8.1	235	2 I54490	tumor necrosis fac
15	133.5	8.0	233	1 S24642	tumor necrosis fac
16	133	7.9	185	2 S52715	tumor necrosis fac
17	133	7.9	232	1 S12606	tumor necrosis fac
18	129.5	7.7	235	2 JU0029	tumor necrosis fac
19	129.5	7.7	306	2 I49139	lymphotoxin-beta -
20	117	7.0	244	2 A46066	lymphotoxin beta -
21	115.5	6.9	193	2 S06192	tumor necrosis fac
22	103.5	6.2	340	2 S49742	hypothetical prote
23	103	6.1	3848	2 T17414	trpc protein - sli
24	99.5	5.9	440	2 T23649	hypothetical prote
25	99	5.9	440	2 I49681	glyceroldehyde-3-p
26	97	5.8	450	2 S38114	hypothetical prote
27	95.5	5.7	553	2 B55514	dihydropyrimidine
28	94	5.6	1486	1 B40333	collagen alpha 1(I
29	93.5	5.6	205	1 QWHDX	lymphotoxin alpha

30	92.5	5.5	197	1 JH0309	tumor necrosis fac
31	92	5.5	549	2 JCS926	secreted klotho pr
32	92	5.5	785	2 T23456	hypothetical prote
33	92	5.5	1012	2 JCS925	membrane klotho pr
34	90.5	5.4	658	2 T39500	serine/threonine-s
35	90.5	5.4	750	2 E84475	probable Athila re
36	90.5	5.4	952	2 AC0447	probable insectici
37	90	5.4	3011	1 S40770	genomg polyprotein
38	89	5.3	1694	2 S50065	sialoadhesin - mou
39	88.5	5.3	202	1 B27303	tumor necrosis fac
40	88.5	5.3	477	2 I38409	adenyl cyclase-a
41	88.5	5.3	1547	2 JQ0096	hypothetical 176K
42	88	5.3	347	2 H75253	hypothetical prote
43	88	5.3	560	1 JQ1221	probable 60K inner
44	88	5.3	1420	2 T37781	probable cytoskele
45	88	5.3	2774	2 A43359	microtubule-associ

ALIGNMENTS

RESULT 1

S53090

CD40 ligand - bovine

C:Species: Bos primigenius: taurus (cattle)

C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999

C:Accession: S53090

R:Mertens, B.E.L.C.; Muriuki, M.

submitted to the EMBL Data Library, February 1995

A:Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.

A:Reference number: S53090

A:Accession: S53090

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-261 <MER>

A:Cross-references: EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g732570

Query Match 11.1% Score 185.5; DB 2; Length 261;

Best Local Similarity 25.1% Pred. No. 5.4e-08;

Matches 75; Conservative 50; Mismatches 111; Indels 63; Gaps 15;

QY	32	PAPSAPAPAPPAA	RSRMFLALGLG	GOVVCSTALF	LYFRAQMDPNRIS	SDSTHCYR	90
DB	8	PSPRSVATGPP	--VSMKIFMYLL	TVFLITQMG	SALFAVILHRLD	--KIEDER	57
QY	91	ILRLHE	-----NAGLQD	STLESEDTLP	DCSRMKAQFQ	GAQVQELQHV	139
DB	58	--NLHEDFVFMKT	IQRCNKGE	SLSL	-----NCEIRSF	EDLVKDINQ	104
QY	140	SGAPAMEGSW	LDVAQRGKPA	QPAFAH	LITNAASIPSG	SHKVTLS	197
DB	105	KKKEKNE	-----MHKGDQ	EPQIAARV	-----ISEASS	KTSVLTQWAP	152
QY	198	MTLSNGK	-LRVNQDGFY	LYANICF	-RHEHSGSV	PTDYLQIMVY	253
DB	153	VTLENGQLAV	KVRGFFIY	ITQVTCN	REFLSQAP	-----FIASL	204
QY	254	LMKGGSTKNN	SGNEFEHFY	SINVGFFK	LRAGEEIS	IQVSNPS	312
DB	205	LLRAANTH	--SSSRKPGQ	QSIIHLG	VFELQSGA	SFVNVPD	261

RESULT 2

A49266

fas ligand - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: A49266

R:Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.

Cell 75, 1169-1178, 1993

A:Title: Molecular cloning and expression of the Fas ligand, a novel member of the

A:Reference number: A49266; MUID:94084792; PMID:7505205

A:Accession: A49266

QY 237 LAMVYVKTISIKIPSHNLKMGSTKNWSEPHFYINVGFFKLRAGEISIQVSNPS 296
 Db 207 LSHVYMRNSKYPODLVME-GRMSTCTTGOMWARSYLGAVENTSADHLVNVSELS 265
 QY 297 LLDPODQATYFGAFKV 312
 Db 266 LVNFEESQTFGLYKL 281

RESULT 5

CD40 ligand - human
 N:Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
 C:Accession: S28017, JH0793; S26694; S28852; I53476; S25684; S30593
 R:Jolienbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; WBO J. 11, 4313-4321, 1992
 A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for CD40
 A:Reference number: S28017; MUID:93049181; PMID:1385114
 A:Accession: S28017
 A:Molecule type: mRNA
 A:Residues: 1-261 <HOL>
 A:Cross-references: EMBL:Z15017; NID:g38483; PIDN:CAAY78737.1; PID:g38484
 R:Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T. J. Exp. Med. 176, 1543-1550, 1992
 A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin synthesis
 A:Reference number: JH0793; MUID:93094757; PMID:1281209
 A:Accession: JH0793
 A:Molecule type: mRNA
 A:Residues: 1-261 <SPR>
 A:Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412
 A:Experimental source: peripheral blood T-cell
 R:Graef, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Krocsek, R.A. Eur. J. Immunol. 22, 3191-3194, 1992
 A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
 A:Reference number: S26694; MUID:93076854; PMID:1280226
 A:Accession: S26694
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-261 <GRA>
 A:Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270
 R:Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J. FEBS Lett. 315, 259-266, 1993
 A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of expression
 A:Reference number: S28852; MUID:93138085; PMID:7678552
 A:Accession: S28852
 A:Molecule type: mRNA
 A:Residues: 1-261 <GAU>
 A:Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124
 A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
 C:Genetics:
 A:Gene: GDB:CD40LG; HIGM1; IMD3
 A:Cross-references: GDB:I20632; OMIM:308230
 A:Map position: Xq26-Xq26
 C:Keywords: glycoprotein; transmembrane protein
 F:13-44/Domain: transmembrane #status predicted <TM>
 F:45-261/Domain: extracellular #status predicted <EXT>
 F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.28; Score 171.5; DB 2; Length 261;
 Best Local Similarity 25.28; Pred. No. 8e-07;
 Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;

QY 33 APSAPAPAPPPAASRSFALIGLIGLGVCSIALF-IYFRAQMDPNRISDSTHCFYRI 91
 Db 9 SPSSAATGLP--ISMKIFMYLLTVFLITQMGTSALFAYLLHRLD--KIEDER----- 57
 QY 92 LRLHE-----NAGLQDSTLESDTLPSDCRRMKQAFQAGVOKELQHVGPQRS 140
 Db 58 -NLHEDFVFMKTIQRCNTGERSLSLL-----NCEIKSQFEGFV-KDIM-----LN 101

QY 141 GAPAMGGSWLDVAQRKPEAQPPAHLITINAASIPSGSHKVTLSSTWTHDRQWAKISN--M 198
 Db 102 KEETKENSE--ENQKGDQNPQIAAHV-----ISEASSKTSVLQWAEKGYTTSNMLV 153
 QY 199 TLSNGK-LRVNODGFYLYANICF-RHETSGSVPTDYQLQWVYVVKTSIKIPSSH--L 254
 Db 154 -TLENGKQLTVKROGLYIYAQVTFCSNREASSQAP-----FIASCLSPGRFERIL 205
 QY 255 MKGSTKNWSEPHFYINVGFFKLRAGEISIQVSNPSLDDPDQDQATYFGAFKV 312
 Db 206 LRAANTH--SSAKPCGQOSIHLGGVFELOPCASVFNVTDFSVSHGTFGTFSGLLKL 261

RESULT 6

S21738
 CD40 ligand - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
 C:Accession: S21738
 R:Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.M.; Spriggs, M.K.
 A:Title: Molecular and biological characterization of a murine ligand for CD40.
 A:Reference number: S21738; MUID:92244364; PMID:1374165
 A:Accession: S21738
 A:Molecule type: mRNA
 A:Residues: 1-260 <ARM>
 A:Cross-references: EMBL:X65453; NID:g50351; PIDN:CAA46448.1; PID:g50352
 C:Keywords: glycoprotein; transmembrane protein
 F:23-46/Domain: transmembrane #status predicted <TM>
 F:47-260/Domain: extracellular #status predicted <EXT>
 F:239/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.48; Score 157; DB 2; Length 260;
 Best Local Similarity 24.88; Pred. No. 1.3e-05;
 Matches 75; Conservative 51; Mismatches 105; Indels 72; Gaps 16;

QY 32 PAPSAPAPPPAASRSFALIGLIGLGVCSIALF-IYFRAQMDPNRISDSTHCFYRI 90
 Db 8 PSRSVATGLP--ASMKIFMYLLTVFLITQMGTSALFAYLLHRLD--KVEEE----- 56
 QY 91 IRLHE-----NAGLQDSTLESDTLPSDCRRMKQAFQAGVQ-----KELQHV 134
 Db 57 -VNLEHEDFVFIKKLRCKNGKSGLSLL-----NCEEMRQFEDLVKIDITLKE----- 103
 QY 135 GPQFSGAPAMGGSWLDVAQRKPEAQPPAHLITINAASIPSGSHKVTLSSTWTHDRQWAK 194
 Db 104 -----EKKENSF--EMQGEDDPOIAAHVYSEA-----NSNAASVLQWAEKGYTM 147
 QY 195 ISNMT-LSNGK-LRVNODGFYLYANICF-RHETSGSVPTDYQLQWVYVVKTSIK--IP 249
 Db 148 KSNLVMLENGKQLTVKREGLYVYVTVTFCSNREPSQRP-----FIVGLWLKPSIG 199
 QY 250 SSHNLKMGSTKNWSEPHFYINVGFFKLRAGEISIQVSNPSLDDPDQDQATYFGA 309
 Db 200 SERILLKAAANTHSSQLCEQQ--SVHLGGVFELOPCASVFNVTDFSVSHGTFGTFSGLLKL 257
 QY 310 FKV 312
 Db 258 LKL 260

RESULT 7

J01344
 tumor necrosis factor alpha precursor - horse
 N:Alternate names: cachectin; TNF alpha
 C:Species: Equus caballus (domestic horse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: J01344
 R:Su, X.; Morris, D.D.; McGraw, R.A.
 A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor alpha precursor
 A:Reference number: J01344; MUID:92084125; PMID:1748301

A:Molecule type: mRNA
A:Residues: 1-235 <EN>
A:Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085
R:Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima,
Nucleic Acids Res. 13, 4417-4429, 1985
A>Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic
A:Reference number: A23127; MUID:85242112; PMID:2989794
A:Accession: A23127
A:Molecule type: mRNA
A:Residues: 1-235 <FRA>
R:Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A>Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide re
A:Reference number: A34251; MUID:89380231; PMID:2777790
A:Accession: A34251
A:Molecule type: protein
A:Residues: 70-87 <CSE>
R:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A>Title: Identification of a common nucleotide sequence in the 3'-untranslated reg
A:Reference number: I59058; MUID:86149365; PMID:2419912
A:Accession: I59058
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-230, 'R', 232-235 <RES>
A:Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083
R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A>Title: Characterization of high molecular weight glycosylated forms of murine tun
A:Reference number: A36696; MUID:91097531; PMID:2268312
A:Accession: A36696
A:Molecule type: protein
A:Residues: 80-85, 'X', 87-99 <SHE>
C:Genetics:
A:Introns: 62/3; 81/1; 97/1
A>Note: The first intron occurs in the 5'-untranslated region
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage
F:80-235/Product: tumor necrosis factor #status experimental <WAT>
F:20/Binding site: myristate (lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (ser) (covalent) #status predicted
F:86/Binding site: carbohydrate (asn) (covalent) #status predicted
F:148-179/Disulfide bonds: #status predicted

Query Match 8.7%; Score 146.5; DB 1; Length 235;
Best Local Similarity 25.6%; Pred. No. 8.5e-05;
Matches 51; Conservative 36; Mismatches 67; Indels 45; Gaps 11;

QY 133 IVGPQR-----SCAP-----AMMEGSWLVDVARGPEAQPPFAHLTINAASIPSGSHKVTLS- 184
 :||||| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 55 VIGPQRKEFPNGLPILSSMAQTLLRSSONSDD-KPVARVVAN-----HQVEEQL 105
 :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 185 SWYHDGWAKISN-MTLNSGKLRYNQDGFYYLANICFRHHRTSGSVPTDYLOLMYTVVK 243
 :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 106 EWLQSORALLIANGMDLKNLVVPADGLIVTSQVLFK-----GGCCPDYV-LLTHTVS 159
 :||||| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 244 -----TSIKIPSSHNLKMGGSKWNKSSEPHFYSYINVGCPFLKRAGEISI 290
 ::||| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 160 RFALSYOEKVNLISAVKSPCKDTPEGALKPW-----YEPIYLGGVFOLEKGDLISA 212
 :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 291 QVSNPSLID-PDODATYFG 308
 :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 213 EVNLPKYLDPAESQVTFG 231
 :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

RESULT 9
S22052
tumor necrosis factor alpha precursor - baboon
C:Species: Papio sp. (baboon)
C:date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: S22052
R:Sanjanwala, M.; Edwards, A.

submitted to the EMBL Data Library, September 1991

A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A:Reference number: S22052

A:Accession: S22052

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 <SAN>

A:Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA4068.1; PID:g38160

C:Genetics:

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:19/20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 8.6%; Score 143.5; DB 1; Length 233;
Best Local Similarity 25.6%; Pred. No. 0.00015;
Matches 50; Conservative 36; Mismatches 70; Indels 39; Gaps 11;

QY 133 IVGPOR--FSGAPAMMGESWLDVAQRK---PEAQPPAHLTINAASIPSGSHKVTLSWY 187

Db 55 VIGPQREFFDPSLI--SPLAQAVRSSRTPSDKPVAVVAN-----PQAEQL---QWL 105

QY 188 HDRGWAKISN-WTLSNGKLRVNDQGYLYLANICFRHETSGSVPTDYLQL-----M 238

Db 106 NRRANALLANGVELRDNLQVPSGLYLYISQVLEK-----GQCPCSTHVLTTISRIA 161

QY 239 VTVVK-----TSIKIPSSHNLKMGSTKNWGNSEFHFYSINVGFFKLRAGEEISIQVN 294

Db 162 SYQTKVNLLSAISKPCQRETPEGAERKPW-----YEPIYLGGVFQLEKGRDLSAE 214

QY 295 PSLLD-PDQDATYFG 308

Db 215 PDYLDFAESGQVYFG 229

RESULT 10

JH0529

tumor necrosis factor alpha precursor - sheep

N:Alternate names: cachectin; TNF alpha

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: JH0529; S48118; S13114; S20661

R:Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with

A:Reference number: JH0529; MUID:92112044; PMID:1765267

A:Accession: JH0529

A:Molecule type: mRNA

A:Residues: 1-234 <GRE>

A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A:Experimental source: alveolar macrophage

R:Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A:Reference number: S48118; MUID:92155784; PMID:1786996

A:Accession: S48118

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-234 <NAS>

A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807

R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.

Nucleic Acids Res. 18, 6723, 1990

A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A:Reference number: S13114; MUID:91067496; PMID:2251151

A:Accession: S13114

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-62,64-234 <YOD>

A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A>Note: comparison with the introns of homologous sequences suggest that this is probabl

C:Superfamily: tumor necrosis factor

C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein;
F:1-77/Domain: propeptide #status predicted <PRO>

F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F:20/Binding site: myristate (Lys) (covalent) #status predicted

F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141; DB 1; Length 234;

Best Local Similarity 25.8%; Pred. No. 0.00024;

Matches 51; Conservative 31; Mismatches 72; Indels 44; Gaps 11;

QY 133 IVGPORFSGAPAMMGESWLDVAQRGPEAQPPAHLTINAASIPSG---SHKVTLSWYH 188

Db 55 VIGPQREPOSPA-----GPFNRPLVQ--TLRSSQASNNKPKVAVVANISAPG 101

QY 189 DRGWA-KISNWTLSNG-KLRVNDQ---DGFTYLYLANICFRHH-----ETSGSVP 231

Db 102 QLRWGDSTANALMANGVELKDQLVVPDGLYLYISQVLEGRGCPSTPLFLTHTSRIA 161

QY 232 TDYQLQMVTVKTSIKIPSSHNLKMGSTKNWGNSEFHFYSINVGFFKLRAGEEISIQ 291

Db 162 VSY-QTKVNL-SAIKSPCHRETLEGAERKPW-----YEPIYQGVFQLEKGRDLSAE 212

QY 292 VSNPSLLD-PDQDATYFG 308

Db 213 INLPEYLDFAESGQVYFG 230

RESULT 11

S11688

tumor necrosis factor alpha precursor - cat

C:Species: Felis silvestris catus (domestic cat)

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000

C:Accession: S11688

R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.

Nucleic Acids Res. 18, 5563, 1990

A:Title: Gene sequence of feline tumor necrosis factor alpha.

A:Reference number: S11688; MUID:91016860; PMID:2216740

A:Accession: S11688

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 <MCG>

A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777

C:Genetics:

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:19/20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 8.4%; Score 140; DB 2; Length 233;

Best Local Similarity 25.1%; Pred. No. 0.00029;

Matches 50; Conservative 35; Mismatches 74; Indels 40; Gaps 10;

QY 124 GAVQKELQHVGPQRFSGAPAMMGESWLDVAQRGKPEAQPPAHLTINAASIPSGSHKVT 183

Db 57 GPQREELPH--GLQLINLPQTLRSS-----SRTPSDKPVAVVAN---PEAEGLQ 104

QY 184 SSWYHGRGAKISN-WTLSNGKLRVNDQGYLYLANICFRHETSGSVPTDYLQL----- 237

Db 105 LS---RRANALLANGVELTDNLKVPDGLYLYISQVLF-----TGQCPSTHVLTTA 157

QY 238 ---WTVVVK---TSIKIPSSHNLKMGSTKNWGNSEFHFYSINVGFFKLRAGEEISI 290

Db 158 RFAVSTQTKVNLSSAISKPCQRETPEGAERKPW-----YEPIYLGGVFQLEKGRDLS 210

QY 291 QVSNPSLLD-PDQDATYFG 308

Db 211 EINLPAYLDFAESGQVYFG 229

RESULT 12

**NUBRO
POCKET**

tumor necrosis factor alpha precursor [validated] - human

N:Alternate names: cachectin; TNFA
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R:R:Medwin, G.E.; Naylor, S.L.; Sakauchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, I.
Nucleic Acids Res. 13, 6361-6373, 1985
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chromosomal location
A:Reference number: A93585; MUID:86016093; PMID:2995927
A:Accession: A93585
A:Molecule type: DNA
A:Residues: 1-233 <NED>
A:Cross-references: GB:X02910; GB:X02910; MID:g37209; PIDN:CAA26669.1; PID:g37210
R:Irish, F.J.M.; Bouguieret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A:Reference number: S36152; MUID:93272029; PMID:8499947
A:Accession: S36153
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-233 <IRI>
A:Cross-references: EMBL:215026; MID:g37211; PIDN:CAA78745.1; PID:g37212
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A:Title: Human tumour necrosis factor: precursor structure, expression and homology to
A:Reference number: A93351; MUID:85086244; PMID:6392892
A:Accession: A93351
A:Molecule type: mRNA
A:Residues: 1-233 <PEN>
A:Cross-references: GB:X02910; GB:X02910; MID:g37309; PIDN:CAA26669.1; PID:g37210
A:Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloid
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.;
Science 228, 149-154, 1985
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A:Reference number: A44189; MUID:85142190; PMID:3856324
A:Accession: A44189
A:Molecule type: mRNA
A:Residues: 1-62, 'S', '64-233 <WAN>
A:Cross-references: GB:M10988; MID:g39737; PIDN:AAA61198.1; PID:g39738
R:Fukuda, S.; Ando, S.; Sanou, O.; Tantai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Ar
Lymphokine Res. 7, 175-185, 1988
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A:Reference number: A61478; MUID:88301617; PMID:2841543
A:Accession: B61478
A:Molecule type: protein
A:Residues: 83-102; 109-119; 121-128, 'X', 130-131; 142-144, 'X', 146, 'XX', 150-152; 159-174; 180
R:Marinout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
ur. J. Biochem. 152, 515-522, 1985
A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A:Reference number: I53311; MUID:86030296; PMID:3932069
A:Accession: I53311
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-233 <MAR>
A:Cross-references: GB:M26331; MID:g339763; PIDN:AAA36758.1; PID:g339764
A:Experimental source: U-937 cells
R:R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurlimoto, M.
ur. J. Biochem. 235, 431-437, 1996
A:Title: O-Glycosylated species of natural human tumor necrosis factor-alpha.
A:Reference number: S62610; MUID:96202967; PMID:8631363
A:Accession: S62610
A:Molecule type: protein
A:Residues: 77-99 <TAK>
R:D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter region
A:Reference number: I54522; MUID:94102809; PMID:7903959
A:Accession: I54522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Note: this sequence differs from that shown in having a Gln inserted between residues R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990

A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-A:Reference number: JH0309; MUID:91065534; PMID:2249779

A:Accession: J50727

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-62, Q, 63-234 <SHA>

A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756

C:Genetics:

A:Introns: 62/3; 80/1; 96/1

C:Superfamily: tumor necrosis factor

F:1-81/Domain: propeptide #status predicted <PRO>

F:82-234/Product: tumor necrosis factor #status predicted <MAT>

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:83/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:147-178/Disulfide bonds: #status predicted

Query Match 8.2%; Score 137.5; DB 1; Length 234;

Best Local Similarity 22.6%; Pred. No. 0.00048;

Matches 68; Conservative 31; Mismatches 99; Indels 103; Gaps 12;

QY 27 EGPLHAPSAPAPAPPPAASR-----SMFLALLGLGLGVGVCSIALFLYFRAQMDPNRIS 81

DB 14 EGPL-----PKAGGPGQSKKCLCLSLFSLVAGATTLC-----LLHFRVIGPQEEES 63

QY 82 EDSTCFYRLRLHBNAGLDSTLESDLPDCRRMKAFOGAVOKLOHIVGPQRFSG 141

DB 64 PNNHLV-----NPVAQMVLRS-----ASRALSDKPLAHVV----- 95

QY 142 APAMMEGSLDVAQRGKPEAOPFAHLTINAAIPSGSHKVTLSWYHGRGWAQISN-MTL 200

DB 96 ANPQVESQ-----LQWLSQRANALLANGNKL 121

QY 201 SNGKRVNDGGYLYLANICFRHETSGVPTDYQLQVMYVVKTSIKIPSSHNLKMG--- 257

DB 122 TQNLVVPADGLYLYSQVLF-----SGQGRSVYLLTHTVSFRFAVSYPKNVNLISAIS 176

QY 258 -----GSTKNKSGNSEFHYISINVGCFKLRAGEISIQVSNPSLLD-PDQDATVF 307

DB 177 PCHRETPAEAPMAW-----YEPIYLGCVFQLEKGRDLSTEVNOPEYLDLAESQVTF 229

QY 308 G 308

DB 230 G 230

RESULT 14

154490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000

C:Accession: 154490

R:Crew, M.D.; Filipowsky, M.E.

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leu

A:Reference number: 154490; MUID:92218012; PMID:1348497

A:Accession: 154490

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 <RES>

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:

A:Gene: FITNF

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 8.1%; Score 135.5; DB 2; Length 235;

Best Local Similarity 25.1%; Pred. No. 0.0007;

Matches 51; Conservative 31; Mismatches 68; Indels 53; Gaps 10;

QY 133 IVGPQRFSGAP-----AMMEGSLDVAQRGKPEAOPFAHLTINAAIPSGSHKVTLSWY 185

DB 55 VIGPQREEKFPNNLPIIGSSMAQTLTLRSSQSSSD-KPAHVAVAN-----HQVDEQL 105

QY 186 WYHGRGWAQISNMTLSNG-KLRVNO-----DGFYLYLANICFRHETSGSVPTDYQLQVM 239

DB 106 EWLRSRG-----ANALLANGMDLKNOLVVPADGLYLYVSVQLFKGQCSYV-----LIT 155

QY 240 YVVK-----TSIKIPSSHNLKMGKSTKNWGSNSEFHYISINVGCFKLRAGE 286

DB 156 HVSFSAVYEDKVNLLSAIKSPCKFETPEGSELAPW-----YEPIYLGCVFQLEKGD 208

QY 287 EISIQVSNPSLLD-PDQDATYFG 308

DB 209 RLSAEVNLPKYLDFAESQVTFG 231

RESULT 15

S24642

tumor necrosis factor alpha precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: 146047; S24642

R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxi

A:Reference number: 146046; MUID:94083525; PMID:8260599

A:Accession: 146047

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-233 <CL>

A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C:Genetics:

A:Gene: TNFA

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

F:20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 8.0%; Score 133.5; DB 1; Length 233;

Best Local Similarity 25.8%; Pred. No. 0.001;

Matches 51; Conservative 30; Mismatches 72; Indels 45; Gaps 11;

QY 133 IVGPQR--FSGAPAMMEGSLDVAQRGKPEA---QFAHLTINAAIPSGSHKVTLSWY 187

DB 55 VIGPQREEKFPNNLPIIGSSMAQTLTLRSSQSSSNKPAHVAVAD-----INSPG 100

QY 188 HDRGWAQISNMTLSNG-KLRVNO-----DGFYLYLANICFRHH-----ETSGSV 231

DB 101 QLRWDSYANALMANGKLEDNOLVVPADGLYLYVSVQLFKGQCSPTPLFTHHTLSRIA 160

QY 232 TDYQLQVMYVVKTSIKIPSSHNLKMGKSTKNWGSNSEFHYISINVGCFKLRAGEISIQ 291

DB 161 VSY-QTKVNL-SAIKSPCHRETPAEAKPW-----YEPIYQGVFQLEKGRDLRS 211

QY 292 VSNPSLLD-PDQDATYFG 308

DB 212 INLPDYLDYAESQVTFG 229

Search completed: April 16, 2003, 12:20:42

Job time : 15.5 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:16:16 ; Search time 9.5 Seconds
(without alignments)

1379.634 Million cell updates/sec

Title: US-09-787-126-6

Perfect score: 1675

Sequence: 1 MRRASRDYGYKLSSEPMGS.....LLDPDQDATYGFAPKVQDID 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	1 TN11_MOUSE	O35235 m tumor nec
2	1597	95.3	318	1 TN11_RAT	O9ese2 r tumor nec
3	1417.5	84.6	317	1 TN11_HUMAN	O14788 h tumor nec
4	258.5	15.4	281	1 TN10_HUMAN	P50591 homo sapien
5	244	14.6	291	1 TN10_MOUSE	P50592 mus musculus
6	188.5	11.3	261	1 TNF5_CALJA	Q9bdn3 callithrix
7	185.5	11.1	261	1 TNF5_BOVIN	P51749 bos taurus
8	183	10.9	278	1 TNF6_RAT	P36940 rattus norv
9	182.5	10.9	261	1 TNF5_AOTTR	Q9bdm3 aotus trivi
10	182	10.9	279	1 TNF6_MOUSE	P41047 mus musculus
11	179.5	10.7	282	1 TNF6_PIG	Q9bea8 sus scrofa
12	178	10.6	280	1 TNF6_MACMU	Q9myl6 macaca mula
13	177	10.6	280	1 TNF6_CERTO	Q9bdn1 cercocebus
14	176.5	10.5	261	1 TNF5_MACMU	Q9bdc7 macaca mula
15	173.5	10.4	281	1 TNF6_HUMAN	P48023 homo sapien
16	171.5	10.2	261	1 TNF5_HUMAN	P29965 homo sapien
17	168.5	10.1	272	1 TNF5_CHICK	Q918d8 gallus gall
18	164	9.8	260	1 TNF5_FELCA	O97605 felis silve
19	159.5	9.5	261	1 TNF5_PIG	O95mq5 sus scrofa
20	157	9.4	234	1 TNFA_CAVPO	P51435 cavia porce
21	157	9.4	260	1 TNF5_MOUSE	P27548 mus musculus
22	154	9.2	260	1 TNF5_CANFA	O97626 canis fami
23	151	9.0	240	1 TNF5_MACNE	Q9bdm7 macaca neme
24	149	8.9	234	1 TNFA_HORSE	P29553 equus cabal
25	148.5	8.9	233	1 TNFA_MACFA	P79337 macaca fasc
26	147.5	8.8	233	1 TNFA_MACMU	P48094 macaca mula
27	147.5	8.8	310	1 TNFC_MARMO	Q9jmi0 marmota mon
28	146.5	8.7	235	1 TNFA_MOUSE	P06804 mus musculus
29	146.5	8.7	239	1 TN14_MOUSE	Q9qyh9 mus musculus
30	145	8.7	260	1 TNF5_RAT	O9z2v2 rattus norv
31	143.5	8.6	233	1 TNFA_PAPHU	O77510 papio hamad
32	143.5	8.6	233	1 TNFA_PAPSP	P33620 papio sp. (
33	141	8.4	234	1 TNFA_SHEEP	P23383 ovis aries

RESULT 1

ID	TN11_MOUSE	1 STANDARD;	PRT;	316 AA.
AC	O35235; O35306; Q9RIY0; Q9JJK8; Q9JJK9;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor) (OCIF).			
GN	TNFSF11 OR RANKL OR TRANCE OR OPGL.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Hybridoma;			
RX	MEDLINE=97460112; PubMed=9312132;			
RA	Wong B.R., Rho J., Arron J., Robinson E., Orlick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.;			
RA	"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";			
RL	J. Biol. Chem. 272:25190-25194 (1997).			
RP	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Thymic lymphoma;			
RX	MEDLINE=98032977; PubMed=9367155;			
RA	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Galibert L.;			
RA	"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";			
RL	Nature 390:175-179 (1997).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=98227661; PubMed=9568710;			
RA	Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.;			
RA	"Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation.";			
RL	Cell 93:165-176 (1998).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Bone marrow stroma;			
RX	MEDLINE=98188248; PubMed=9520411;			
RA	Yasuda H., Shima H., Nakagawa N., Yamaguchi K., Kinosaki M., Mochizuki S.-I., Tomoyasu A., Yan K., Goto M., Murakami A., Tsuda E., Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;			

34	140	8.4	174	1 TN15_HUMAN	O95150 homo sapien
35	140	8.4	233	1 TNFA_FELCA	P9101 felis silve
36	139.5	8.3	233	1 TNFA_CANFA	P51742 canis fami
37	139.5	8.3	233	1 TNFA_HUMAN	P01375 homo sapien
38	139	8.3	234	1 TNFA_CAPHI	P13296 capra hircu
39	137	8.2	235	1 TNFA_RABIT	P04924 oryctolagus
40	135.5	8.1	235	1 TNFA_PERLE	P36939 peromyscus
41	134.5	8.0	240	1 TN14_HUMAN	Q03557 homo sapien
42	133.5	8.0	233	1 TNFA_BOVIN	O06599 bos taurus
43	133	7.9	232	1 TNFA_PIG	P23563 sus scrofa
44	129.5	7.7	233	1 TNFA_MARMO	O35734 marmota mon
45	129.5	7.7	235	1 TNFA_RAT	P16599 rattus norv

ALIGNMENTS

Db 241 VVKTSIKIPSSHNLMKGGSTKNWGNSEHFYSINVGFFKLGRAGEEISQVSNPSLLDP 300

QY 301 DQDATYFGAFKVDQDID 316

Db 301 DQDATYFGAFKVDQDID 316

RESULT 2

TN11_RAT STANDARD; PRT; 318 AA.

AC Q9ESE2; Q91Z19; (Rel. 41, Last annotation update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).

DE TNFSF11 OR RANKL OR TRANCE OR OPGL.

IS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Tibial bone;

RX MEDLINE=20540945; PubMed=11092398;

RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S., Zheng M.H.;

RT "Cloning, sequence and functional characterization of the rat homologue of receptor activator of NF-kB ligand.";

RL J. Bone Miner. Res. 15:2178-2186(2000).

RN [2]

RP SEQUENCE OF 266-318 FROM N.A.

RC STRAIN=Fischer 344;

RX PubMed=11804028;

RA Odgren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savas A., Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y., Marks S.C. Jr.;

RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";

RL Int. J. Dev. Biol. 45:853-859(2001).

CC -1- FUNCTION: Cytokine that binds to TNFSF11B/OPG and to TNFSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcaemia of malignancy.

CC -1- SUBUNIT: Homotrimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).

CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.

CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

CC -----

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CC -----

CC EMBL; AF187319; AAC17031.1; .

CC EMBL; AF425669; AAL23963.1; .

CC HSP; P50591; ID0G

CC InterPro; IPR003636; TNF_ab.

CC InterPro; IPR000478; TNF_family.

CC Pfam; PF00229; TNF; 1.

CC ProDom; PD002012; TNF_ab; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF_1; FALSE_NEG.

DR PROSITE; PS0049; TNF_2; 1.

KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;

KW Signal-anchor.

FT CHAIN 1 318 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, MEMBRANE FORM.

FT CHAIN 141 318 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, SOLUBLE FORM.

FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 69 318 EXTRACELLULAR (POTENTIAL).

FT SITE 140 141 CLEAVAGE (BY SIMILARITY).

FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 264 264 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 317 317 I -> M (IN REF. 2).

SQ SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CRC64;

Query Match 1 95.3%; Score 1597; DB 1; Length 318;

Best Local Similarity 95.0%; Pred. No. 7.2e-125;

Matches 302; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 MRRASRDYGYLRSSEMGSGPGVPHGGLHPAPAPAPAPPAPPPAASRSMFLALGLGLGQ 60

Db 1 MRRASRDYGYLRSSEMGSGPGVPHGGLHPAPAPAPAPPAPPPAASRSMFLALGLGLGQ 60

QY 61 VCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLQDSTLESDT--LPDSCRRM 118

Db 61 VCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLQDSTLESDTLEALPDSCRRM 120

QY 119 KQAFQAVQKELQHVGPQRFSGAPAMMGESWLDVAQRKPEAOPFAHLITNAASIPSGS 178

Db 121 KQAFQAVQKELQHVGPQRFSGVPMAMMGESWLDVAQRKPEAOPFAHLITNAADIPSGS 180

QY 179 HKYTLSSWYHGRGWAKISNNTLSNGKLKRVNODGYLYLYANICFRHHETSGSVPTDYQLM 238

Db 181 HKYTLSSWYHGRGWAKISNNTLSNGKLKRVNODGYLYLYANICFRHHETSGSVPTDYQLM 240

QY 239 VYVVKTSIKIPSSHNLMKGGSTKNWGNSEHFYSINVGFFKLGRAGEEISQVSNPSLL 298

Db 241 VYVVKTSIKIPSSHNLMKGGSTKNWGNSEHFYSINVGFFKLGRAGEEISQVSNPSLL 300

QY 299 DPQDATYFGAFKVDQDID 316

Db 301 DPQDATYFGAFKVDQDID 318

RESULT 3

TN11_HUMAN

ID TN11_HUMAN STANDARD; PRT; 317 AA.

AC O14788; O14723; Q9P2Q3; Q96Q17;

DT 16-OCT-2001 (Rel. 40, Created)

DT 15-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).

GN TNFSF11 OR RANKL OR TRANCE OR OPGL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Bone marrow, and Peripheral blood;

RX MEDLINE=98032977; PubMed=9367155;

RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,

RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,

RA Galibert L.;

RT "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";

EMBL; AF013171; AAC51762.1; -.
 EMBL; AB037599; BAA90488.1; -.
 DR HSP; P50591; IDOG.
 Genew; HGNC:11926; TNFSF11.
 MIM; 602642; -.
 DR InterPro; IPR003636; TNE_abc.
 DR InterPro; IPR000478; TNE_family.
 Pfam; PF00229; TNE; 1.
 DR ProDom; PD002012; TNE_abc; 1.
 DR SMART; SM00207; TNE; 1.
 DR PROSITE; PSQ0251; TNE_1; FALSE_NEG.
 DR PROSITE; PS50049; TNE_2; 1.
 KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
 FW Signal-anchor; Alternative splicing.
 CHAIN 1 317
 FT
 CHAIN 140 317
 FT
 DOMAIN 1 47
 TRANSMEM 48 68
 FT
 DOMAIN 69 317
 SITE 139 140
 FT CARBOHYD 171 171
 FT CARBOHYD 198 198
 FT CARBOHYD 1 47
 VARSPLIC 1 73
 CONFLICT 194 194 A -> G (IN REF. 4).
 SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;

Query Match 84.6%; Score 1417.5; DB 1; Length 317;
 Best Local Similarity 84.3%; Pred. No 5e-110;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY	1	MRRASRDYGYKLSSSEMGGPGVPHGPIHPAPSAPAPAPPAAASRMFLALGLGLQG	60
DB	1	MRERASDYTYKLGSEMGCGPGAPHEGPLH-APPPPAHQPPAASRMFVALGLGLQG	59
QY	61	VVCISALFYFRAMPDPNRISTSTHCFFYLRLRHENAGLDQSTLESED--LPDSCRM	118
DB	60	VVCUSVALFFRAMPDPNRISEDGTCHCIYILRLHENDFDQTILESDQTKLIIPDCNRI	119
QY	119	KOAFQAVOKELQHIVGPQRFGSAPAMEGSWLDVAQRPKEAQPFPAHLTINAASIPSGS	178
DB	120	KOAFQAVOKELQHIVGSOHRAEKAEMVDGSLDLAKRKLEAQPFPAHLTNATIDPSGS	179
QY	179	HKYTLSWSYHDRGWAKINSMTLSNGKLVRNQDFYYILYANICFHHSHTSGVPDYQLQM	238
DB	180	HKVLSLSWYHDRGWAKINSMTFNKGKLVNQDFYYILYANICFRHHETSGDLAYEQLQM	239
QY	239	VYVYKTSIKIPSSHNLKMGGSTKNWSCNSEFHFTSYNVGGFFFKLRAGEEISIQVSNPSSL	298
DB	240	VYVYKTSIKIPSSHNLKMGGSTKYWSCNSEFHFTSYNVGGFFFKLRSGEEISIEVSNPSSL	299
QY	299	DPQDATYGFCAFKVDID 316	
DB	300	DPQDATYGFCAFKVRDI 317	

RESULT 4
 TN10_HUMAN
 ID TN10_HUMAN STANDARD; PRT; 281 AA.
 AC P50591;
 DT 01-OCT-1996 (Rel. 34, Created)
 DE 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
 GN TNFSF10 OR TRAIL OR APO2L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI TaxID=9606;

[1] SEQUENCE FROM N.A.
 RX MEDLINE-96111955; PubMed-8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF
 family that induces apoptosis.";
 RL Immunology 3:673-682(1995).
 [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-96278649; PubMed-8663110;
 RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
 RA Ashkenazi A.;
 RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
 necrosis factor cytokine family.";
 RL J. Biol. Chem. 271:12687-12690(1996).
 [3]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 RX MEDLINE-20017054; PubMed-10549288;
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 complex with death receptor 5.";
 RL Mol. Cell 4:563-571(1999).
 [4]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RX PubMed-10542098;
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Sreaton G.R.;
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 specificity in apoptotic initiation.";
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 [5]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RX MEDLINE-99413670; PubMed-10485660;
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 RA Sung Y.C., Oh B.-H.;
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
 selective antitumor activity.";
 RL Immunify 11:253-261(1999).
 CC -|- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 possibly also to TNFRSF1B/OPG. Induces apoptosis. Its activity
 may be modulated by binding to the decoy receptors
 TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF1B/OPG that cannot
 induce apoptosis.
 CC -|- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 trimer.
 CC -|- SUBUNIT: Homotrimer.
 CC -|- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -|- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
 AND PROSTATE
 CC -|- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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 RX EMBL: U37518; AAC50332.1;
 RX EMBL: U57059; AAB01233.1;
 RX Genbank: HGNC:11925; TNFSF10.
 RX NIM: 603598;
 RX PDB: 1D0G; 22-OCT-99.
 RX PDB: 1D4V; 01-NOV-99.
 RX PDB: 1D2Q; 11-FEB-00.
 RX InterPro: IPR003636; TNF_abc.
 RX InterPro: IPR000478; TNF_family.

DR Pfam: PF00229; TNF: 1.
 DR ProDom: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF: 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS0049; TNF_2; 1.
 KW Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
 ZINC: 3D-structure. 17
 FT DOMAIN 1 18 38
 FT TRANSMEM 18 38
 FT CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT METAL 230 230
 FT ZINC.
 FT SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;
 Query Match 15.4%; Score 258.5; DB 1; Length 281;
 Best Local Similarity 26.4%; Pred. No. 3e-14;
 Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
 QY 43 PAASRSMELALGLGQVVCYSIALFLYFRAQMD--PNRISDSTHCFYRLRLHENAGL 100
 DB 10 PSLGTCVLIVITVLLQSLCVAVTYFTNELKQMDKYSGGIACF-----LKEDDSY 64
 QY 101 QDSTLESDTLPSQCRMKQAFQGVOK-----ELQHVGPQFSGAPAMM 146
 DB 65 WDP--NDESMNSPCVQWQVWQLRQLVKMLRTSETISTVQEKQNI SPL----- 113
 QY 147 EGSWLDVAQRGPEAOPFAHLT-----INAAISPSGSHKVTL-----SSWYHDR-GWAKIS 196
 DB 114 -----VREGRQVRA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSHSFLS 165
 QY 197 NMTLSNGKLRVNDQGFYLYANICPRHETSGVPTDYQLQLVVYVTKTSKIPSSHNLMK 256
 DB 166 NLHLRNGELVILHEKGYIYISOTYFRQBEIKENTKNDKQMVQYIYKYT-SYDPDILLMK 224
 QY 257 CGSTKNMNSGFHFYSINWGGFFKLAGEEISIQVSNPSLLDPDQDAYFYGAKV 312
 DB 225 SARNSCWSDAEVGLYSIYQGIFELKENDRIFSVYTNELHIDMDHEASFFGAFV 280
 RESULT 5
 ID TN10_MOUSE STANDARD; PRT; 291 AA.
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96111955; PubMed-8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF
 family that induces apoptosis.";
 RL Immunology 3:673-682(1995).
 CC -|- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 possibly also to TNFRSF1B/OPG. Induces apoptosis. Its activity
 may be modulated by binding to the decoy receptors
 TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF1B/OPG that cannot
 induce apoptosis.
 CC -|- SUBUNIT: HOMOTRIMER (By similarity).
 CC -|- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -|- TISSUE SPECIFICITY: WIDESPREAD.
 CC -|- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR EMBL; U37522; AAC52345.1; -
 DR HSSP; P50591; IDOG.
 DR MGD; MGI:107414; Tnfzf10.
 DR InterPro; IPR003636; TNF_abc.
 DR InterPro; IPR000478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS0049; TNF_2; 1.
 KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 14.6%; Score 244; DB 1; Length 291;
 Best Local Similarity 27.5%; Pred. No. 4.9e-13;
 Matches 83; Conservative 50; Mismatches 111; Indels 58; Gaps 15;

OY 52 ALLGLGLGQ-----VVCSTAL-----FLYFRAQMD--PNRISDSTHCFYRIL 92
 DB 6 ALKDLFSQHFHFMVICIVLLQVAVVYTFYIMEMKQLQDNYSKIGLACFSK-- 63
 OY 93 RLHENAGLDSTLESDTLPSDC-----RRMKAQFAGVQKEQLHIV--PQFSGAPAMM 146
 DB 64 ---TDEDWDST--DGEILNRCLQVKRQLYLIEVILRTFDQISVPEKQLSTPPLP 118
 OY 147 EGSWLDVAQRGPEAQPFAHLT-----INAAISPSGSHKVTL-----SSWYDR-GWAKIS 196
 DB 119 RG-----GRPO-KVAHRTGTRRSNSALIPISKDKTLGQIESWESSRKGHSFLN 169
 OY 197 NMTLSNGLRVNODGFYLYANICRHHF--TSQVPTDYL--OLMYVYVTKSIKIPS 250
 DB 170 HVLFRNGELVIEQEGYLIYSOTYFRQEAQDAKMWKDKVTKQLVQIYIKYT-STPD 228
 OY 251 SHNLKGGSTKNSGNSEPHFYSINVGFFKLRAGEISIQVSNPDLDPDQDATYFGAF 310
 DB 229 PIVLMKSARNCSWRDAEYGLSYIYGGFLFELKKNDRIFSVYTNELMDLDQEAFFGAF 288
 311 KV 312
 DB 289 LI 290

RESULT 6
 TNF5_CALJA STANDARD; PRT; 261 AA.
 ID TNF5_CALJA
 AC Q9BDN3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
 DE L) (CD154 protein).
 GN TNF5F5 OR CD40LG OR CD40L.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 OC Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;

RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
 CC proliferation in the absence of co-stimulus as well as B-cell
 CC production in the presence of IL-4. Involved in immunoglobulin
 CC class switching (By similarity).
 CC -!- SUBUNIT: HOMOTRIMER (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR EMBL; AF344844; AAK37603.1; -
 DR HSSP; P29965; ITALY.
 DR InterPro; IPR003263; TNF_5.
 DR InterPro; IPR003636; TNF_abc.
 DR InterPro; IPR000478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_abc; 1.
 DR ProDom; PD008600; TNF_5; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS0049; TNF_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 261 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT CHAIN 113 261 MEMBER 5, MEMBRANE FORM.
 FT FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT FT MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
 FT FT CYTOPLASMIC (POTENTIAL).
 FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT FT (POTENTIAL).
 FT FT EXTRACELLULAR (POTENTIAL).
 FT FT SITE 112 113 CLEAVAGE (BY SIMILARITY).
 FT FT DISULFID 178 218 POTENTIAL.
 FT FT CARBOHYD 240 240 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 261 AA; 29360 MW; 10CA588D923754EB CRC64;

Query Match 11.3%; Score 188.5; DB 1; Length 261;
 Best Local Similarity 25.8%; Pred. No. 1.7e-08;
 Matches 77; Conservative 49; Mismatches 110; Indels 63; Gaps 16;

OY 32 PAPSAPAPAPPAASRSMFLALLGLGQVGVCSIALF-LYFRAQMDPNRISDSTHCFYR 90
 DB 8 PVPRAATGPP--VSMKIFWLLTVLTITQMGTSALFAVILHRLD--KIEDER----- 57
 OY 91 ILRLHE-----NAGLDSTLESDTLPSDCRRMKQAQFAGVQKEQLHIVGPORF 139
 DB 58 --NLHEDFVFMKTIQRCNTGERSLSLL-----NCEIKSQFEGFV-KDIM-----L 100
 OY 140 SGAPAMMEGSWLDVAQRGPEAQPFAHLT-----INAAISPSGSHKVTLSWYDRGWAKISN-- 197
 DB 101 NKEEKKKNSF--EMQKQDNQPIAAHV-----ISEASSKTSVLQWAEKGYTMSNNL 152
 OY 198 MTLNSGLK-LRVNODGFYLYANICF--RHETSGSVPTDYQLMWVYVYVTKSIKIPSSHN-- 253
 DB 153 VYLENGKQLTVRRQGLYIYIYQVTFCSNREASSQAP-----FIASLCPLPPNFERI 204
 OY 254 LMKGGSTKNSGNSEPHFYSINVGFFKLRAGEISIQVSNPDLDPDQDATYFGAFV 312
 DB 205 LLRAANTH--SSAKPCGQSIHLGGIFELQPGASVFNVTDFQVSHGTFSTFGLKL 261

```
RESULT 7
TNF5_BOVIN
ID TNF5_BOVIN STANDARD; PRT; 261 AA.
AC P51749.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-
DE related activation protein) (TRAP) (T cell antigen GP39).
GN TNF5 OR CD40LG OR CD40L.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
C TISSUE=Blood;
RX MEDLINE=96006582; PubMed=7590981;
RA Mertens B.E.L.C., Muriuki M., Gaidulis L.;
RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
RT and tumor necrosis factor alpha.";
RL Immunogenetics 42:430-431(1995).
CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IgE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; 248469; CAAB8363.1; -
DR HSSP; P29965; ITALY.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 261
FT CHAIN 113 261
FT CHAIN 261
FT DOMAIN 1 22
FT TRANSMEM 23 46
FT DOMAIN 47 261
FT SITE 112 113
FT DISULFID 178 218
FT CARBOHYD 240 240
FT SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787FD CRC64;
Query Match 11.1%; Score 185.5; DB 1; Length 261;
Best Local Similarity 25.1%; Pred. No. 3e-08;
Matches 75; Conservative 50; Mismatches 111; Indels 63; Gaps 15;
QY 32 PAPSAPAPAPPAASRSMFLALIGLIGLQGVCSIALF-LYFRAQMDPNRISDTHCFYR 90
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Db 8 PSRSVATGPP--VSMKIFMYLLTVLITQIMIGSALEFAVYLHRLD--KIEDER----- 57
QY 91 ILRLHE-----NAGLDSTLESDTLDPSCRMKQAFQAGVOKELQHVGPQRF 139
Db 58 --NLHEDFVPMKTIQRCNKGEGSL--NCEIRSRFEDLVKIDMN-----REV 104
QY 140 SGAPAMWGSWLDVAORGKPEAPFAHLTINAAISPGSHKVTLSWYHQRGNALISN-- 197
Db 105 KKEKNFE-----MKRGDQEPQIAAHV-----ISEASSKTTSLVQWAPRGYTTLSNNL 152
QY 198 MTLNNGK-LRVNODGFYLLYANICF-RHETSGVSPDYQLQWVYVVKTSIKIPSSN-- 253
Db 153 VTLENGQLQAVKRGQFYIYTVTCNRETLSQAP-----FIASLCIKSPSGERI 204
QY 254 LMGGSSTKNWGNSEFHYISNVGGFKRAGEEISIQVSNPSLLDPDQATYFGAKV 312
Db 205 LLRAANTH--SSSKPCQOSIHGGVPELOSGASVFVNTDPQSVSHGTGTSGLLKL 261

RESULT 8
TNF6_RAT
ID TNF6_RAT STANDARD; PRT; 278 AA.
AC P36940.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE ligand).
GN TNFRF6 OR FASL OR APTLGL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=94084792; PubMed=7505205;
RA Suda T., Takahashi T., Golstein P., Nagata S.;
RT "Molecular cloning and expression of the Fas ligand, a novel member
RT of the tumor necrosis factor family.";
RL Cell 75:1169-1178(1993).
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC modulates its effects (By similarity).
CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC KIDNEY AND LUNG.
CC -!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
DR EMBL; U03470; AAC52129.1; -
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_abc; 1.
```


DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE ligand).
GN TNFSF6 OR FASL OR APTLIG1 OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand."
RL Cell 76:969-976(1994).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RX STRAIN=C57BL/6;
RA Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family."
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster."
RL Immunity 1:131-136(1994).
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RX STRAIN=BALB/c;
RA Fenner M.H., Shioda T., Isselbacher K.J.;
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids."
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RX STRAIN=C3H; TISSUE=Spleen;
RA Ayrolidi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,
RA Cannarile L., Miglioni G., Delfino D.V., Riccardi C.;
RT "Cloning and expression of a short Fas ligand: A new alternatively
RT spliced product of the mouse Fas ligand gene."
RL Blood 94:3456-3467(1999).
RN [6]
RN CHARACTERIZATION OF VARIANT GLD.
RX MEDLINE=96091792; PubMed=7495745;
RA Hahne M., Peitsch M.C., Imler M., Schroeter M., Lowin B.,
RA Rousseau M., Bron C., Renno T., French L., Tschopp J.;
RT "Characterization of the non-functional Fas ligand of gld mice."
RL Int. Immunol. 7:1381-1386(1995).
RN [7]
RN VARIANT'S ALA-184 AND GLY-218.
RX STRAIN=Various;
RA Published=9108079;
RA Kiyagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,
RA Yagita H.;
RT "Polymorphism of murine Fas ligand that affects the biological
RT activity."
RL Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC modulates its effects (By similarity).

CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
CC Secreted (isoforms FASL and FASLs).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLs; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS
CC WHILE ISOFORM FASLs PREVENTS APOPTOSIS INDUCED BY FAS/FASL
CC INTERACTION.
CC -1- PFM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
CC LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
CC RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC EMBL; U06948; AAA17800.1;
CC EMBL; U10984; AAA19778.1;
CC EMBL; S76752; AAB33780.1;
CC EMBL; U58995; AAB02915.1;
CC EMBL; AF119335; AAD52106.1;
CC HSSP; P01375; 4T5V.
CC MGD; MGI:99255; Tnfsf6.
CC InterPro; IPR003636; TNF_abc.
CC InterPro; IPR000478; TNF_family.
CC Pfam; PF00229; TNF; 1.
CC PRODOM; PD002012; TNF_abc; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS50049; TNF_2; 1.
CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
CC Disease mutation; Polymorphism; Alternative splicing.
CC CHAIN 1 279 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC MEMBER 6, MEMBRANE FORM.
CC CHAIN 128 279 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
CC DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 4 69 PRO-RICH.
CC DOMAIN 45 51 POLY-PRO.
CC SITE 127 128 CLEAVAGE (BY SIMILARITY).
CC DISULFID 200 231 POTENTIAL.
CC CARBOHYD 117 117 N-LINKED (GLCNAC... (POTENTIAL).
CC CARBOHYD 182 182 N-LINKED (GLCNAC... (POTENTIAL).
CC CARBOHYD 248 248 N-LINKED (GLCNAC... (POTENTIAL).
CC CARBOHYD 258 258 MISSING (IN ISOFORM FASL).
CC VARSPLIC 1 210 T -> A (IN STRAINS BALB/C AND DBA;
CC VARIANT 184 184 ENHANCES CYTOTOXICITY).
CC VARIANT 218 218 E -> G (IN STRAINS BALB/C AND DBA;
CC VARIANT 273 273 F -> L (IN GLD; ABOLISHES BINDING OF FASL
CC TO ITS RECEPTOR).
CC SEQUENCE 279 AA; 31442 MW; 379722728E0A1CA CRC64;
CC Query Match 10.9%; Score 182; DB 1; Length 279;
CC Best Local Similarity 22.7%; Pred. No. 6.3e-08;
CC Matches 72; Conservative 48; Mismatches 105; Indels 92; Gaps 13;
CC QY 13 RSSEMGSGGVPHGPHLPAPSAPAPAP-----PAASRSMFLALLGLG 57
CC Db 38 RGPQRRPPPPPPVSP-PPPSQPLPLPLPKKKDHNTNLWLPLVFFVFLVALVGMG 96
CC QY 58 LGQVVCISIALFLYFRQMDPNRISESTCTCFRILRLHFNAGLQDSTLSEDTLPSCRR 117

RESULT 12
TNF6_MACMU STANDARD; PRT; 280 AA.

AC Q9ML6; Q9BDM5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN TNFSF6 OR FASL OR CD95L.
OS Macaca mulatta (Rhesus macaque).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
[1] SEQUENCE FROM N.A.
[2] SPECIES=M.mulatta; TISSUE=Lymphocytes;
[3] MEDLINE=21383618; PubMed=11491535;
[4] Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
[5] Weiss W.R., Ansari A.A.;
[6] "Cloning, sequencing, and homology analysis of nonhuman primate
[7] Fas/Fas-ligand and co-stimulatory molecules.";
[8] Immunogenetics 53:315-328(2001).
[9]
[10] SEQUENCE FROM N.A.
[11] SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
[12] Kiril I., Inoue T., Yoshino K.;
[13] Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[14] -1- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
[15] transduces the apoptotic signal into cells. May be involved in
[16] cytotoxic T cell mediated apoptosis and in T cell development.
[17] TNFSF6/FAS-mediated apoptosis may have a role in the induction of
[18] peripheral tolerance, in the antigen-stimulated suicide of mature
[19] T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3
[20] modulates its effects (By similarity).
[21] -1- SUBUNIT: Homotrimer (Potential).
[22] -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
[23] similarity).
[24] -1- PTM: The soluble form derives from the membrane form by
[25] proteolytic processing (By similarity).
[26] -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
[27]
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[34] or send an email to license@isb-sib.ch).
[35]
[36] EMBL; AF344856; AAK37539.1; -
[37] EMBL; AB035138; BAA90294.1; -
[38] EMBL; AB035139; BAA90295.1; -
[39] EMBL; AB035140; BAA90296.1; -
[40] HSSP; P01375; 4TSV.
[41] InterPro; IPR003636; TNF_abc.
[42] InterPro; IPR000478; TNF_family.
[43] Pfam; PF00229; TNF; 1.
[44] PRINTS; PR01234; TNCRSISFCT.
[45] ProDom; PD002012; TNF_abc; 1.
[46] SMART; SM00207; TNF; 1.
[47] PROSITE; PS00251; TNF_1; 1.
[48] PROSITE; PS50049; TNF_2; 1.
[49] Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
[50] CHAIN 1 280
[51] MEMBER 5, MEMBRANE FORM.
[52] TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
[53] CHAIN 129 280
[54] TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
[55] MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
[56] CYTOPLASMIC (POTENTIAL).
[57] DOMAIN 1 80
[58] TRANSMEM 81 101
[59] SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT DOMAIN 102 280 (POTENTIAL).
FT DOMAIN 4 69 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 45 64 PRO-RICH.
FT SITE 129 129 POLY-PRO.
FT SITE 201 232 CLEAVAGE (BY SIMILARITY).
FT DISULFID 201 232 POTENTIAL.
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 60 60 S -> P (IN REF. 1).
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;
Query Match 10.68; Score 178; DB 1; Length 280;
Best Local Similarity 22.08; Pred. No. 1.4e-07;
Matches 68; Conservative 44; Mismatches 105; Indels 92; Gaps 10;
QY 22 PGVHEGHPAPAP--APPPAASRS-----MFLALGLGLGQWVCS 65
DB 46 PPPPPPPPLPPPPSPPLPLPLPKKGNHSTGLCLVPMFVVALVGLGLG----- 99
QY 66 ALFLYFRACMDPNRISESTHCFYRLILHFNAGLQDSTLESDTLPDSCRRMKAFOGA 125
DB 100 -MFQLFHLQ-----KELAELESTSQKHTA-----SS 125
QY 126 VOKELQHVGPORFSGAPAMMGSLDVAQRCKPAQPFALHT--INAAIPSGSHKVT 183
DB 126 LEKQIGHPSPPE-----KKQRVAHLTGKPNRSM----- 158
QY 184 SSWYHGRGWAKISNMTLSNGLRVNODGFYLYANICFRHETSGVPTDYQLQWVYVK 243
DB 159 LEWEDTYGLVLUSGVYKKGGLVINETGLYFYKSVFQGQCTN-----LPLSHKVYM 212
QY 244 TSIKIPSSHNLMKGGSTKNWNSGFHYFYSINVGGFFKLRAGEEISIQVSNPDLDPDQD 303
DB 213 RNSKYPQDILVME-KGMNSYCTTGQWVAHSSYLGAVFNLTADSHLVVNVSELSLVNFEES 271
QY 304 ANYFGAFKV 312
DB 272 QTFFGLYKL 280
RESULT 13
TNF6_CERTO STANDARD; PRT; 280 AA.
AC Q9BDN1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN TNFSF6 OR FASL OR CD95L.
OS Cercocobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercocobus.
OX NCBI_TaxID=9531;
RN [1]
[1] SEQUENCE FROM N.A.
[2] TISSUE=Lymphocytes;
[3] MEDLINE=21383618; PubMed=11491535;
[4] Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
[5] Weiss W.R., Ansari A.A.;
[6] "Cloning, sequencing, and homology analysis of nonhuman primate
[7] Fas/Fas-ligand and co-stimulatory molecules.";
[8] Immunogenetics 53:315-328(2001).
[9] -1- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
[10] transduces the apoptotic signal into cells. May be involved in
[11] cytotoxic T cell mediated apoptosis and in T cell development.
[12] TNFSF6/FAS-mediated apoptosis may have a role in the induction of
[13] peripheral tolerance, in the antigen-stimulated suicide of mature
[14] T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3
[15] modulates its effects (By similarity).
[16] -1- SUBUNIT: Homotrimer (Probable).

Search completed: April 16, 2003, 12:19:00
Job time : 10.5 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:16:42 ; Search time 28 Seconds
(without alignments)
2325.389 Million cell updates/sec

Title: US-09-787-126-6

Perfect score: 1675
Sequence: 1 MRRASRDYGYKLSSEMGs.....LLDPDQATYFGAFKVDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	263.5	15.7	214	13 Q9DDZ5	Q9ddz5 brachydanio
2	217.5	13.0	287	13 Q90WT9	Q90wt9 gallus gall
3	149	8.9	234	6 Q9TTJ3	Q9ttj3 equus caball
4	142	8.5	232	4 Q9UIV3	Q9uiv3 homo sapien
5	133.5	8.0	215	11 Q99ND1	Q99nd1 tamiasciuru
6	133	7.9	157	4 Q43647	O43647 homo sapien
7	132	7.9	149	6 Q97543	Q97543 actus nancy
8	132	7.9	217	11 Q9ERG6	Q9erg6 peromyscus
9	131.5	7.9	156	11 Q91ZL4	Q91zl4 sigmodon hi
10	131	7.8	149	6 Q97538	Q97538 actus vocif
11	131	7.8	149	6 Q9TTG8	Q9ttg8 actus nigri
12	130	7.8	216	11 Q70332	Q70332 mesocricetu
13	127.5	7.6	217	6 Q9BEC5	Q9bec5 tenrec ecan
14	126.5	7.6	217	6 Q9BEG1	Q9beg1 bradypus tr
15	126.5	7.6	217	6 Q9BEG0	Q9beg0 cyclopes di
16	126	7.5	216	6 Q9BEC9	Q9bec9 ochotona pr

17	125.5	7.5	235	11 Q9J127	Q9j127 rattus norv
18	123.5	7.4	138	6 Q9TTG7	Q9ttg7 actus lemur
19	122.5	7.3	215	6 Q9BEB8	Q9beb8 erinaceus e
20	122.5	7.3	235	11 Q9J126	Q9j126 rattus norv
21	120.5	7.2	217	6 Q9BEF4	Q9bef4 cabassous u
22	118.5	7.1	216	6 Q9BEC4	Q9bec4 talpa europ
23	114.5	6.8	432	11 Q9ESV6	Q9esv6 rattus norv
24	103	6.1	3848	5 Q76737	Q76737 dictyosteli
25	102	6.1	169	11 Q9WV90	Q9wv90 marmota mon
26	101.5	6.1	246	13 Q9I976	Q9i976 oncorhynch
27	101.5	6.1	246	13 Q9I970	Q9i970 oncorhynch
28	101.5	6.1	962	16 Q8XX7	Q8xx7 ralstonia s
29	101	6.0	216	6 Q9BEO0	Q9beo0 macropus ru
30	100.5	6.0	551	6 Q8WP18	Q8wp18 macaca fasc
31	100.5	6.0	1014	6 Q8WP17	Q8wp17 macaca fasc
32	99.5	5.9	558	5 Q45692	Q45692 caenorhabdi
33	97	5.8	255	13 Q9DEP9	Q9dep9 oncorhynch
34	97	5.8	325	5 Q9V5G2	Q9v5g2 drosophila
35	96	5.8	408	16 Q9LW7	Q9lwn7 rhizobium l
36	96	5.7	1485	13 Q9I171	Q9i171 xenopus lae
37	95	5.7	1012	4 Q9UEF7	Q9uef7 homo sapien
38	94	5.6	891	1 Q93635	Q93635 thermococcu
39	93	5.6	93	6 Q9TTJ2	Q9ttj2 bos taurus
40	92.5	5.5	214	6 Q9BEE3	Q9bef3 didelphis m
41	92	5.5	294	2 Q53921	Q53921 synchococc
42	92	5.5	549	4 Q9Y4F0	Q9y4f0 homo sapien
43	92	5.5	785	5 Q9XUS7	Q9xus7 caenorhabdi
44	92	5.5	1012	4 Q9UEI9	Q9uei9 homo sapien
45	91	5.4	218	11 Q9DAT2	Q9dat2 mus musculu

ALIGNMENTS

RESULT 1

Q9DDZ5 PRELIMINARY; PRT; 214 AA.

AC Q9DDZ5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE TRAIL-like protein.
GN TNFSF10L.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Bobe J., Goetz F.W.;

RT "Molecular cloning and expression of a TNF receptor and two TNF

ligands in the fish ovary."

RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).

DR EMBL; AF250041; AAG47640.1;

DR HSSP; P50591; IDOG.

DR ZFIN; ZDB-GENE-010801-1; tnfsf10l.

DR InterPro; IPR003636; TNF_abc.

DR Pfam; PF00229; TNF; 1.

DR ProDom; PD002012; TNF_abc; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00049; TNF-2; 1.

SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match 15.7%; Score 263.5; DB 13; Length 214;

Best Local Similarity 31.5%; Pred. No. 3.3e-15;

Matches 69; Conservative 42; Mismatches 77; Indels 31; Gaps 6;

QY 117 RMKQAFQAVQKQLHQHVQRFSGAPAMNE-----GS--WLDVAQGRKPEAQAHLTI 169

DB 2 KLAEGIKAYISKVTSIISKQTLHARTQTHSYNTGSKFMTVMQR-----PSAHLTL 55

QY 170 NAASIPS-----GSHKVTLSWYHGRGAKISNMTLSNGKLRVNDQGYFL 215
 DB 56 SSASONSPOSMDHQPQDFLEHSCRPVHTWANKSFGHLYNNTLNGKLRVNDQGYFL 115
 QY 216 YANICFRHETSGVPTDYQLQMLVTV--KTSIKIPSSHNLMKGGSTKNWNSSEFHYFS 273
 DB 116 YSQVTFYRPSDSQSSVSHQLVCYIKTKSYLNP1--QLLKGVGTRCWAPDAEVALHS 173
 QY 274 INVGGFFKLAGEEISIOVNSPLDPPDQATYFCAKV 312
 DB 174 VTQGLFELRAGDEVFSVSSPTWYGEDSSSYFCAFL 212

RESULT 2

Q90WT9 PRELIMINARY; PRT; 287 AA.
 AC Q90WT9;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE TNF-related apoptosis inducing ligand.
 Gallus gallus (Chicken).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 DR Bridgman J.T., Johnson A.L.;
 RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
 ovary."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY057941; AAL23702.1;
 DR InterPro; IPR0003636; TNF_family.
 DR ProDom; PD002012; TNF_abc; 1.
 DR PROSITE; PS00229; TNF; 1.
 DR PROSITE; PS0049; TNF_2; 1.
 DR PROSITE; PS0049; TNF_2; 1.
 SQ SEQUENCE 287 AA; 32092 MW; DB06ELC95087B108 CRC64;

Query Match 13.0%; Score 217.5; DB 13; Length 287;
 Best Local Similarity 26.7%; Pred. No. 5.4e-11;
 Matches 66; Conservative 51; Mismatches 103; Indels 27; Gaps 8;

QY 81 SEDSTHCYRILRLHNLNAGLDSTLESDTLFDCRRMKQAFQAGVQKELHIVGPQFES 140
 DB 51 SSELRCQLNQOEGNLEE--LISN-----QSCCLKANTIKAYVATVTENVISRSYVN 104
 QY 141 GAPAMEGSWLDVAQ--RGKPEAQPFALHTI---NAASIPSG-----SHKVTLSGW 186
 105 EA----QKSYFNISEGVATYTLGRPSAHLFRPQNPADGSSRRFGLNLSQSCRHAYRW 160
 QY 187 YHGRGAKISNMTLSNGKLRVNDQGYFLYANICFRHHETSGVPTDYQLQMLVTV--VKT 245
 DB 161 EDSTHSLONITTYDGRGLRVNQAGYVYVQIVRYSDRGAGARVSPVQLVQCNWKT 220
 QY 246 IKIPSSHNLMKGGSTKNWNSSEFHYFSINWGGPKLAGEISIOVNSPLDPPDQAT 305
 DB 221 YSQPL--LLKGVGTRCWAPDAEYGLHALYOGGLFELKAGDELFSVSSLAIDYSDAAS 278
 QY 306 YFGAFKV 312
 DB 279 YFGAFRL 285

RESULT 3

Q9TTJ3 PRELIMINARY; PRT; 234 AA.
 AC Q9TTJ3;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Tumor necrosis factor-alpha.

GN TNFA.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=THOROUGHRED; TISSUE=ARTERIAL ENDOTHELIUM;
 RA Ishida N., Sato F., Hasegawa T.;
 RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB035735; BAA88349.1;
 DR HSSP; P01375; 188M.
 DR InterPro; IPR003636; TNF_abc.
 DR InterPro; IPR000478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00229; TNF_1; 1.
 DR PROSITE; PS0049; TNF_2; 1.
 DR PROSITE; PS0049; TNF_2; 1.
 SQ SEQUENCE 234 AA; 25430 MW; 2384D4950A21F377 CRC64;

Query Match 8.9%; Score 149; DB 6; Length 234;
 Best Local Similarity 24.18; Pred. No. 4.1e-05;
 Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

QY 133 IVGPQFSGAPAMEGSWLDVAQKQ-----PEAQPFALHTINAASIPSGSHKVTLSWY 187
 DB 55 VIGPQREQLPNAQF--SINPLAQLTLSSRTSPDRVAHVAN-----PQAEGL---QWL 106
 QY 188 HGRGAKISN-MTSLNGKLRVNDQGYFLYANICFRHHETSGVPTDYQLQMLVTVVKT 246
 DB 107 SGRNALLANGVLTDLNQLVPLDGLYLYISOVLEK---GQCPSTHVLTHITISRLAV 162
 QY 247 KIPSSHNLMKG-----GSTKNWNSSEFHYFSINWGGPKLAGEISIOVSN 294
 DB 163 SYPSKVNLSAISKSLANTESPQAEAKPW-----YEPIYLGGVFQLEKGDLSABINQ 215
 QY 295 PSLLD-PPDQATYFG 308
 DB 216 PNYLDFAESGGVYFG 230

RESULT 4

Q9UIV3 PRELIMINARY; PRT; 232 AA.
 AC Q9UIV3;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Tumor necrosis factor.
 GN TNF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93272029; PubMed=8499947;
 RA Iris F., Bougueleret L., Prieur S., Caterina D., Primas G., Perrot V.,
 RA Jurka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.;
 RT "Dense Alu clustering and a potential new member of the NFkappaB
 family within a 90 kilobase HLA class III segment."
 RL Nat. Genet. 3:137-145(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96215741; PubMed=8629302;
 RA Utans U., Quist W.C., McManus B.M., Wilson J.E., Arceci R.J.,
 RA Wallace A.F., Russell M.E.;
 RT "Allograft inflammatory factor-1. A cytokine-responsive macrophage
 molecule expressed in transplanted human hearts."
 RL Transplantation 61:1387-1392(1996).


```
FT NON_TER 1 1
FT NON_TER 215 215
SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E988 CRC64;

Query Match 8.0%; Score 133.5; DB 11; Length 215;
Best Local Similarity 24.3%; Pred. No. 0.00083;
Matches 45; Conservative 30; Mismatches 71; Indels 39; Gaps 7;

QY 133 IVGPORF---SGAPAMGGSHLDVAQRK-PEAQPFALHTINAAIPSGSHKVTLSWTH 188
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 46 VIGPQREFFNNPLPSAQOQLTLRSSQNMNDKPVAVHVAOTE-----EOLWLIS 97
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 DRGWAKISN-WTSLNGKLRVNDGPGYILYANICFRHHETSGSVPTDYLQLMVYVVK--- 243
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 98 RRANALLANGHELINQLVVPADGLYLYISQVLFQGGCSSTV-----LTHHTVSRFV 151
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 244 -----TSIKIPSSHNLKMGSTKNNSGNSEHFHYSINVGPFKLRAGEEISIQVSN 294
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 152 SYQDKVNLSSAIKSPCKRESLEGAEKFW-----YEPYILGGVFFELQKGRLSAEVNL 204
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 295 PSLLD 299
: : : : :
205 PSYLD 209

RESULT 6
O43647 PRELIMINARY; PRT; 157 AA.
AC O43647;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043342; AAC03542.1; -.
DR HSSP; P01375; 1ABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 157 AA; 17380 MW; D1344822267E9F20 CRC64;

Query Match 7.9%; Score 133; DB 4; Length 157;
Best Local Similarity 24.4%; Pred. No. 0.0006;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

QY 159 PEAQPFALHTINAAIPSGSHKVTLSWTHDRGWAKISN-WTSLNGKLRVNDGPGYILYA 217
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 PSDKPVAVHVA-----PQAEGL---QWLNRRANALLANGVELRDNLVVPSEGLYLIYS 60
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 218 NICFRHETSGSVPTDYLQ-----MVYVVK-----TSIKIPSSHNLKMGSTKNNSG 265
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 QVLEK-----GQGCSTHLLTHTISRIAVSYQTKVNLSSAIKSPQRETTPGAEKAPW-- 114
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 266 NSEHFYSINVGPFKLRAGEEISIQVSNPSLLD-PQDATYFG 308
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 -----YEPYILGGVFFELQKGRLSAEINRPDYLDFAESGQVYFG 153
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
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O97543
ID O97543 PRELIMINARY; PRT; 149 AA.
AC O97543;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus nancymae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
RL Identification, cloning and sequencing of different interleukin genes in 4 Aotus species.
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014513; AAD01539.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFA8A CRC64;

Query Match 7.9%; Score 132; DB 6; Length 149;
Best Local Similarity 24.4%; Pred. No. 0.00068;
Matches 40; Conservative 31; Mismatches 61; Indels 33; Gaps 8;

QY 159 PEAQPFALHTINAAIPSGSHKVTLSWTHDRGWAKISN-WTSLNGKLRVNDGPGYILYA 217
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 PSDKPVAVHVA-----PQAEGL---QWLNRRANALLANGVELRDNLVVPSEGLYLIYS 53
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 218 NICFRHETSGSVPTDYLQ-----MVYVVK-----TSIKIPSSHNLKMGSTKNNSG 265
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 54 QVLEK-----GQGCSTHLLTHTISRIAVSYQTKVNLSSAIKSPQRETTPGAEKAPW-- 107
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 266 NSEHFYSINVGPFKLRAGEEISIQVSNPSLLD-PQDATYFG 308
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 108 -----YEPYILGGVFFELQKGRLSAEINRPDYLDFAESGQVYFG 146
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
Q9ERG6 PRELIMINARY; PRT; 217 AA.
ID Q9ERG6;
AC Q9ERG6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Herbst M.M., Schountz T.;
RL Cloning of the deer mouse interferon gamma, interleukin-10 and tumor necrosis factor genes.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307013; AAG30264.1; -.
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
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DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNECROSISFCT.
DR ProDom; PD002012; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;

Query Match
Best Local Similarity 7.9%; Score 132; DB 11; Length 217;
Matches 46; Conservative 31; Mismatches 68; Indels 44; Gaps 8;

QY 133 IVCQRFSGAP-----AMEGSLDVAORGKPEAQPFAHLTINAASIPSGSHKVTLS- 184
DB 47 VIGQREEPNLPPIIGSAQTLTIRSSQSSD-KPVAHVAN-----HQVDEQL 97

185 SMYHDSRGAKISN-WTSLNGKLRVNDGFFYLYANTICFRHETSGSVPTDYQLAVYVVK 243
DB 98 EWLSSRRANALLANGMDLNOLVIPADGLYLVYSQVLFKGGGCSNVY-----LLRHTVS 151

QY 244 -----TSIKIPSSHNLKMGSTKNSGSEHFEYFISVINGGFKLRAGEEISI 290
DB 152 RFVASYEDKVNLSAISKPCPKETPEGSELKPW-----YEPIYLGGVFQLEKGRDLSA 204

QY 291 QVSNPSLLD 299
DB 205 EVNLPKYLVD 213

RESULT 9
QY1ZL4 PRELIMINARY; PRT; 156 AA.
ID Q91ZL4
AC Q91ZL4
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Sigmomon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
AL Blanco J.C., Pieteva L.M., Prince G.A.;
AL "Sigmomon hispidus cytokines, chemokines and interferons.";
AL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF421388; AAL1818.1;
DR InterPro; IPR003636; TNF; 1.
DR InterPro; IPR000478; TNF; 1.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF; 1.
DR PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 156 AA; 17303 MW; DC565F3BC3C82684 CRC64;

Query Match
Best Local Similarity 7.9%; Score 131.5; DB 11; Length 156;
Matches 39; Conservative 27; Mismatches 61; Indels 35; Gaps 6;

QY 162 OPAHLTINAASIPSGSHKVTLSWYHDSRGAKISN-WTSLNGKLRVNDGFFYLYANIC 220
DB 11 KPVAHVYVNAQAEQ-----LEWLSQRANALLANGMDLNOLVIPADGLYLVYSQVL 63

QY 221 FRHETSGSVPTDYQLAVYVVK-----TSIKIPSSHNLKMGSTKNSGNS 267
DB 64 FK-----GLGRSCNLTHTVRSIAVSYEDKVNLSAISKPCPKETPQGAELKPW----- 113

QY 268 EFHETSVINGGFKLRAGEEISIQVSNPSLLD-PDQDATYFG 308
DB 11 KPVAHVYVNAQAEQ-----LEWLSQRANALLANGMDLNOLVIPADGLYLVYSQVL 63
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Db 114 ---YEPIYLGGVFQLEKGRDLSAENVNHPKYLDPAESGQVYFG 152

RESULT 10
QY57538 PRELIMINARY; PRT; 149 AA.
ID Q97538
AC Q97538
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
AL Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
AL "Identification, cloning and sequencing of different interleukin genes
AL in 4 Aotus species.";
AL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014508; AAD01534.1;
DR HSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF; 1.
DR InterPro; IPR000478; TNF; 1.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNECROSISFCT.
DR ProDom; PD002012; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match
Best Local Similarity 7.8%; Score 131; DB 6; Length 149;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

QY 159 PEAPPAHLTINAASIPSGSHKVTLSWYHDSRGAKISN-WTSLNGKLRVNDGFFYLYA 217
DB 1 PSDKPAHVAVAN-----PQAGQL---OWLNRANALLANGVELNDQLVPESEGLYLYS 53

QY 218 NICFRHETSGSVPTDYQLQ-----WYVVK-----TSIKIPSSHNLKMGSTKNSG 265
DB 54 QVLFK-----GCGCSTFMTLTHSIRIAVSQAQVNLSSAISKPCQRETTPRGAKNPW-- 107

QY 266 NSRFHETSVINGGFKLRAGEEISIQVSNPSLLD-PDQDATYFG 308
DB 108 -----YEPIYLGGVFQLEKGRDLSAENVNHPKYLDPAESGQVYFG 146

RESULT 11
QY57538 PRELIMINARY; PRT; 149 AA.
ID Q97538
AC Q97538
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus nigricaps (black-headed night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
AL Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
AL Patarroyo M.E.;
AL "Aotus nigricaps gene for TNF alpha.";
AL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF097328; AAF21303.1;
DR
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DR HSP: P01375; 4TSV
DR InterPro; IPR003636; TNE_abc.
DR InterPro; IPR000478; TNE_family.
DR Pfam; PF00229; TNE; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNE_abc; 1.
DR SMART; SM00207; TNE; 1.
DR PROSITE; PS00251; TNE_1; 1.
DR PROSITE; PS50049; TNE_2; 1.
DR NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match 7.8%; Score 131; DB 6; Length 149;
Best Local Similarity 24.4%; Pred. No. 0.00084;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

QY 159 PEAOFFAHLTINAASIPSGSHKVTLSWYHGRGAKISN-WTSLNGKLRVNDGFFYLVA 217
Db 1 PSDKPAHVAVN---PQEGQL---QWLNRRANALLANGVELRDNLVVPBGLYLVIS 53
218 NICEFRHETSGVPTDYLQ-----MVYVVK-----TSIKIPSSHNLKMGSTKNWSG 265
54 QVLEK-----GQGPCSTFMTLTHSIRIAVSQAQVNLISAIRKSPCQRETPRGAKTNPW-- 107
266 NSEFHYISNVGGFFKLAGEEISIQVNSPLLD-PQDQATVFG 308
108 -----YEPIYLGQVQLERKGRLSAEINLPDYLDAESGVYTFG 146

RESULT 12
O70332 PRELIMINARY: PRT: 216 AA.
AC O70332;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSUE=SPLEEN;
RX MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tyron V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
leishmaniasis."
DR HMBL; AF046215; AAC40100.1;
DR HSP; P06804; 2TNE.
DR InterPro; IPR003636; TNE_abc.
DR InterPro; IPR000478; TNE_family.
DR Pfam; PF00229; TNE; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNE_abc; 1.
DR SMART; SM00207; TNE; 1.
DR PROSITE; PS00251; TNE_1; 1.
DR PROSITE; PS50049; TNE_2; 1.
DR NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 23793 MW; BADA3F83F45B533 CRC64;

Query Match 7.8%; Score 130; DB 11; Length 216;
Best Local Similarity 24.7%; Pred. No. 0.0017;
Matches 46; Conservative 29; Mismatches 71; Indels 40; Gaps 8;

QY 133 IVGPQRFSGAPAMMEGSLDVA---AQRGKPEAQFPAHLTINAASIPSGSHKVTLS-SWY 187
Db 47 VIGPQREKFPPIIGSMQTLFRSSQNSNDKPGHVAVN-----HQVEEQLWL 98
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QY 188 HDGRGAKISN-WTSLNGKLRVNDGFFYLIAICFRHETSGVPTDYLQLVYVVK--- 243
Db 99 SHRANALLANGSLKDNQIVPADGLYLVYSQVLFER-----GQGPCSYV-LTHTVSRIA 152
QY 244 -----TSIKIPSSHNLKMGSTKNWSGNSEFHFYSINVGGFFKLAGEEISIQVS 293
Db 153 VSYEDNVNLLSAIKSPCKETPEGEELKPW-----YEPIYLGQVQLERKGRLSAEIN 205
QY 294 NPSLLD 299
Db 206 LPKYLD 211

RESULT 13
Q9BEC5 PRELIMINARY: PRT: 217 AA.
AC Q9BEC5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Tenrec ecaudatus (tailless tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Tenrec.
OX NCBI_TaxID=94439;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286826; CAC28538.1;
DR HSP; P01375; 4TSV.
DR InterPro; IPR003636; TNE_abc.
DR InterPro; IPR000478; TNE_family.
DR Pfam; PF00229; TNE; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNE_abc; 1.
DR SMART; SM00207; TNE; 1.
DR PROSITE; PS00251; TNE_1; 1.
DR PROSITE; PS50049; TNE_2; 1.
DR NON_TER 1
FT NON_TER 217
SQ SEQUENCE 217 AA; 23845 MW; 1C5013E9B77B54A CRC64;

Query Match 7.6%; Score 127.5; DB 6; Length 217;
Best Local Similarity 24.0%; Pred. No. 0.0028;
Matches 49; Conservative 29; Mismatches 51; Indels 75; Gaps 10;

QY 133 IVGPQRFSGAPAMMEGSLDVAQRGKPEAQ-----PFAHLTINAASIPSGSHK 180
Db 46 VIGPQREKFP-----GSPHLI-----KPLTQTLRSSRTSLSDKPAHVAV--ASTQDSGLK 95
QY 181 VTLSWYHGRGW-AKISNMTLSN-----GKLRVNDGFFYLIAICFRHETSGSVPTD 233
Db 96 -----WVKYANALLDNVQLIDNLPVLDGLYLVYSQVLFKPGCGHGT----- 140
QY 234 YLQLMYYVVKT-----SIKIPSSHNLKMGSTKNWSGNSEFHFYSIN 275
Db 141 -----YVILTHVSRIVSYQAKVNLISAIRKTPCHRETPESSETKPW-----YEPIY 187
QY 276 VGGFFKLAGEEISIQVNSPLLD 299
Db 188 LGGVFQLKGRLSAEINLPNYLD 211

RESULT 14
Q9BEG1 PRELIMINARY: PRT: 217 AA.
AC Q9BEG1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
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RESULT 15
Q9BEGO Q9BEGO PRELIMINARY; PRT; 217 AA.
ID Q9BEGO;
AC Q9BEGO;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Cyclopes didactylus (silky anteater).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.
OX NCBI_TaxID=84074;
[1]
RN SEQUENCE FROM N.A.
RP van Dijk M.A.M., de Jong W.W.;
RT *models indicate that rodents are monophyletic and lagomorphs are
RT their sister group.*;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A7286828; CAC28514.1; -
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR PIRfam; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.

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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:17:27 ; Search time 13.5 Seconds
(without alignments)
688.714 Million cell updates/sec

Title: US-09-787-126-6
Perfect score: 1675
Sequence: 1 MRRASRDYGYLRSSEMGSGPVHGPPLHPPAPSAFAPPPAASRSMFLALGLIGLQ 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	316	2	US-08-842-842-7
2	1675	100.0	316	4	US-08-989-362-2
3	1675	100.0	316	4	US-09-052-521C-2
4	1554	92.8	294	3	US-08-996-139-11
5	1554	92.8	294	4	US-08-995-659-11
6	1554	92.8	294	4	US-09-215-649A-11
7	1554	92.8	294	4	US-09-577-780-11
8	1417.5	84.6	317	3	US-08-996-139-13
9	1417.5	84.6	317	4	US-08-995-659-13
10	1417.5	84.6	317	4	US-09-215-649A-13
11	1417.5	84.6	317	4	US-09-052-521C-4
12	1417.5	84.6	317	4	US-09-577-780-13
13	258.5	15.4	279	4	US-09-072-993C-3
14	258.5	15.4	281	1	US-08-670-354-2
15	258.5	15.4	281	3	US-08-584-031-1
16	258.5	15.4	281	3	US-08-780-496-1
17	258.5	15.4	281	4	US-08-883-086-10
18	258.5	15.4	281	4	US-09-320-424-2
19	258.5	15.4	281	4	US-09-333-593A-6
20	258.5	15.4	281	4	US-09-157-864-11
21	258.5	15.4	281	5	PCR-US96-10895-2
22	244	14.6	291	1	US-08-670-354-6
23	244	14.6	291	1	US-09-320-424-6
24	244	14.6	291	5	PCR-US96-10895-6
25	240	14.3	256	4	US-09-320-424-13
26	236	14.1	253	4	US-09-320-424-11
27	229.5	13.7	177	4	US-09-105-343A-7

28	224	13.4	183	4	US-09-105-343A-8	Sequence 8, Appl1
29	183	10.9	278	4	US-08-339-214-16	Sequence 16, Appl1
30	183	10.9	278	4	US-08-339-214-26	Sequence 26, Appl1
31	182	10.9	279	4	US-08-339-214-24	Sequence 24, Appl1
32	182	10.9	279	4	US-08-339-214-32	Sequence 32, Appl1
33	173.5	10.4	281	2	US-08-810-453-2	Sequence 2, Appl1
34	173.5	10.4	281	3	US-08-815-190A-2	Sequence 2, Appl1
35	173.5	10.4	281	4	US-09-290-640-25	Sequence 25, Appl1
36	173.5	10.4	281	4	US-09-479-524-3	Sequence 3, Appl1
37	173.5	10.4	281	4	US-08-339-214-8	Sequence 8, Appl1
38	173.5	10.4	281	4	US-08-339-214-30	Sequence 30, Appl1
39	173.5	10.4	281	4	US-09-589-287B-6	Sequence 6, Appl1
40	173.5	10.4	281	4	US-09-157-864-10	Sequence 10, Appl1
41	173.5	10.4	281	4	US-09-006-755B-1	Sequence 1, Appl1
42	173.5	10.4	281	5	PCT-US95-00362-2	Sequence 2, Appl1
43	171.5	10.2	261	1	US-07-940-605A-2	Sequence 2, Appl1
44	171.5	10.2	261	1	US-08-184-423-8	Sequence 8, Appl1
45	171.5	10.2	261	1	US-08-360-923A-2	Sequence 2, Appl1

ALIGNMENTS.

RESULT 1
US-08-842-842-7
; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: OSTEOCALCIN BINDING PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeWitt Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,842
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-842-7

Query Match 100.0%; Score 1675; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.7e-157; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0;

QY	1	MRRASRDYGYLRSSEMGSGPVHGPPLHPPAPSAFAPPPAASRSMFLALGLIGLQ	60
DB	1	MRRASRDYGYLRSSEMGSGPVHGPPLHPPAPSAFAPPPAASRSMFLALGLIGLQ	60
QY	61	VVCSIALFLYFRAQMDPNRISESTHCFYRLRLHFNAGLQDSTLESDTLPDSCRMKQ	120
DB	61	VVCSIALFLYFRAQMDPNRISESTHCFYRLRLHFNAGLQDSTLESDTLPDSCRMKQ	120
QY	121	AFQAGVQKQLQHVGPORFSGAPANMEGSLDVAQRKPEAQPFAHLTINAASTPSGSHK	180
DB	121	AFQAGVQKQLQHVGPORFSGAPANMEGSLDVAQRKPEAQPFAHLTINAASTPSGSHK	180

QY 181 VTLSSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQVMY 240
 DB 181 VTLSSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQVMY 240
 QY 241 VVTSIKIPSSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPDLDP 300
 DB 241 VVTSIKIPSSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPDLDP 300
 QY 301 DQDATYGAFAKVQDID 316
 DB 301 DQDATYGAFAKVQDID 316

RESULT 2

US-08-989-362-2
 ; Sequence 2, Application US/08989362
 ; Patent No. 6242586
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorman, Daniel M.
 ; APPLICANT: Mattson, Jeanine D.
 ; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
 ; TITLE OF INVENTION: Reagents
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/989,362
 ; FILING DATE: 12-DEC-1997
 ; CLASSIFICATION: 56
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/032,846
 ; FILING DATE: 13-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ching, Edwin P.
 ; REGISTRATION NUMBER: 34,090
 ; REFERENCE/DOCKET NUMBER: DX0686
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650)852-9196
 ; TELEFAX: (650)496-1204
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 316 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-989-362-2

Query Match 100.0%; Score 1675; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 4.7e-157;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRASRDYGYKLRSEEMSGGVPHEGHPAPSAAPAPPPAASRSMFLALLGLGLGQ 60
 DB 1 MRRASRDYGYKLRSEEMSGGVPHEGHPAPSAAPAPPPAASRSMFLALLGLGLGQ 60
 QY 61 VVCSTALFLYFRAQMDPNRIESTDTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQ 120
 DB 61 VVCSTALFLYFRAQMDPNRIESTDTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQ 120
 QY 121 AFOGAVOKELQHVGPORFSCAPAMMGSLDVAORGKPEAQPPFAHLTINAASIPSGSHK 180
 DB 121 AFOGAVOKELQHVGPORFSCAPAMMGSLDVAORGKPEAQPPFAHLTINAASIPSGSHK 180

QY 181 VTLSSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQVMY 240
 DB 181 VTLSSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQVMY 240
 QY 241 VVTSIKIPSSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPDLDP 300
 DB 241 VVTSIKIPSSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPDLDP 300
 QY 301 DQDATYGAFAKVQDID 316
 DB 301 DQDATYGAFAKVQDID 316

RESULT 3

US-09-052-521C-2
 ; Sequence 2, Application US/09052521C
 ; Patent No. 6316408
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William J.
 ; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
 ; FILE REFERENCE: A-451Bv
 ; CURRENT APPLICATION NUMBER: US/09/052,521C
 ; CURRENT FILING DATE: 1998-03-30
 ; PRIOR APPLICATION NUMBER: 08/880,855
 ; PRIOR FILING DATE: 1997-06-23
 ; PRIOR APPLICATION NUMBER: 08/842,842
 ; PRIOR FILING DATE: 1997-04-16
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-052-521C-2

Query Match 100.0%; Score 1675; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 4.7e-157;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRASRDYGYKLRSEEMSGGVPHEGHPAPSAAPAPPPAASRSMFLALLGLGLGQ 60
 DB 1 MRRASRDYGYKLRSEEMSGGVPHEGHPAPSAAPAPPPAASRSMFLALLGLGLGQ 60
 QY 61 VVCSTALFLYFRAQMDPNRIESTDTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQ 120
 DB 61 VVCSTALFLYFRAQMDPNRIESTDTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQ 120
 QY 121 AFOGAVOKELQHVGPORFSCAPAMMGSLDVAORGKPEAQPPFAHLTINAASIPSGSHK 180
 DB 121 AFOGAVOKELQHVGPORFSCAPAMMGSLDVAORGKPEAQPPFAHLTINAASIPSGSHK 180
 QY 181 VTLSSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQVMY 240
 DB 181 VTLSSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQVMY 240
 QY 241 VVTSIKIPSSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPDLDP 300
 DB 241 VVTSIKIPSSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPDLDP 300
 QY 301 DQDATYGAFAKVQDID 316
 DB 301 DQDATYGAFAKVQDID 316

RESULT 4

US-08-996-139-11
 ; Sequence 11, Application US/08996139
 ; Patent No. 6017729
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Dirk M.
 ; APPLICANT: Galibert, Laurent
 ; APPLICANT: Maraskovsky, Eugene

US-09-215-649A-11
: Sequence 11, Application US/09215649A
: Patent No. 6271349
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: Galibert, Laurent
: Maraskovsky, Eugene
: TITLE OF INVENTION: Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/215,649A
: FILING DATE: 17-Dec-1998
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/996,139
: FILING DATE: <Unknown>
: APPLICATION NUMBER: USN 08/813,509
: FILING DATE: 07 MARCH 1997
: APPLICATION NUMBER: USN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2851-A
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11

Query Match 92.8%; Score 1554; DB 4; Length 294;
Best Local Similarity 99.7%; Pred. No. 3.5e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 GVPHEGLHPAPAPAPPPAASRSMFLALLGLGLGVVCSIALFLYFRAQMDPNRISE 82
DB 1 GVPHEGLHPAPAPAPPPAASRSMFLALLGLGLGVVCSIALFLYFRAQMDPNRISE 60
QY 83 DSTHCFYRILRLHENADLQDSTLESDTLPSDCRRMKQAFQGVQKELQHVGPQFSGA 142
DB 61 DSTHCFYRILRLHENADLQDSTLESDTLPSDCRRMKQAFQGVQKELQHVGPQFSGA 120
QY 143 PAMMEGSLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSWYHDSRWAKISNMTLSN 202
DB 121 PAMMEGSLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSWYHDSRWAKISNMTLSN 180
QY 203 GKLVRNODGYIYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSNLMKGGSTKN 262
DB 181 GKLVRNODGYIYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSNLMKGGSTKN 240
QY 263 WSGNSEFFHYTSINVGFFKLRAGEEISIQVSNPDLDPDQDATYFFGAFKQVDDID 316
DB 241 WSGNSEFFHYTSINVGFFKLRAGEEISIQVSNPDLDPDQDATYFFGAFKQVDDID 294

RESULT 7
US-09-577-780-11
: Sequence 11, Application US/09577780
: Patent No. 6419929
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: Galibert, Laurent
: Maraskovsky, Eugene
: TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/577,780
: FILING DATE: 24-May-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/995,659
: FILING DATE: <Unknown>
: APPLICATION NUMBER: USN 08/813,509
: FILING DATE: 07 MARCH 1997
: APPLICATION NUMBER: USN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2852-A
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-577-780-11

Query Match 92.8%; Score 1554; DB 4; Length 294;
Best Local Similarity 99.7%; Pred. No. 3.5e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 GVPHEGLHPAPAPAPPPAASRSMFLALLGLGLGVVCSIALFLYFRAQMDPNRISE 82
DB 1 GVPHEGLHPAPAPAPPPAASRSMFLALLGLGLGVVCSIALFLYFRAQMDPNRISE 60
QY 83 DSTHCFYRILRLHENADLQDSTLESDTLPSDCRRMKQAFQGVQKELQHVGPQFSGA 142
DB 61 DSTHCFYRILRLHENADLQDSTLESDTLPSDCRRMKQAFQGVQKELQHVGPQFSGA 120
QY 143 PAMMEGSLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSWYHDSRWAKISNMTLSN 202
DB 121 PAMMEGSLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSWYHDSRWAKISNMTLSN 180
QY 203 GKLVRNODGYIYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSNLMKGGSTKN 262
DB 181 GKLVRNODGYIYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSNLMKGGSTKN 240
QY 263 WSGNSEFFHYTSINVGFFKLRAGEEISIQVSNPDLDPDQDATYFFGAFKQVDDID 316
DB 241 WSGNSEFFHYTSINVGFFKLRAGEEISIQVSNPDLDPDQDATYFFGAFKQVDDID 294

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RESULT 8
US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-996-139-13

Query Match      84.6%; Score 1417.5; DB 3; Length 317;
Best Local Similarity 84.3%; Pred. No. 1.1e-131;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYKLSSEEMSGPGVPHEGPHLPAPAPAPPPAASRSMFLALIGLIGLQ 60
Db 1 MRRASRDYTKYLRGSEEMGGPGAPHEGPHLP-APPPAPHPAPPAASRSMFVALLGLGQ 59
QY 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHENAGLDSTLESED--LPDSCRMM 118
Db 60 VVCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFDQTLESQDTKLIPDSCRRI 119
QY 119 KQAFQAVQKELQHIYGVQRFSGAPAMEGSWLDVAQRGKPEAQPPFAHLTINAASIPSGS 178
Db 120 KQAFQAVQKELQHIYGVQSHIRAKAMVDGSLDLAKRSKLEAQPPFAHLTINAADIPSGS 179
QY 179 HKVTLSSWYHRCWAKISNNMTLSNGKLRVNQDGFYLYLANICFRHHETSGSVPTDYQLQM 238
Db 180 HKVTLSSWYHRCWAKISNNMTFSGKLVNQDGFYLYLANICFRHHETSGDLATEYQLQM 239
QY 239 VYVTKTSIKIPSSHTLMKGGSTKYNWGNSEFHYFSINVGFFKLRSGEEISIEVSNPSLL 299
Db 240 VYVTKTSIKIPSSHTLMKGGSTKYNWGNSEFHYFSINVGFFKLRSGEEISIEVSNPSLL 299

RESULT 9
US-08-995-659-13
; Sequence 13, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-995-659-13

Query Match      84.6%; Score 1417.5; DB 4; Length 317;
Best Local Similarity 84.3%; Pred. No. 1.1e-131;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYKLSSEEMSGPGVPHEGPHLPAPAPAPPPAASRSMFLALIGLIGLQ 60
Db 1 MRRASRDYTKYLRGSEEMGGPGAPHEGPHLP-APPPAPHPAPPAASRSMFVALLGLGQ 59
QY 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHENAGLDSTLESED--LPDSCRMM 118
Db 60 VVCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFDQTLESQDTKLIPDSCRRI 119
QY 119 KQAFQAVQKELQHIYGVQRFSGAPAMEGSWLDVAQRGKPEAQPPFAHLTINAASIPSGS 178
Db 120 KQAFQAVQKELQHIYGVQSHIRAKAMVDGSLDLAKRSKLEAQPPFAHLTINAADIPSGS 179
QY 179 HKVTLSSWYHRCWAKISNNMTLSNGKLRVNQDGFYLYLANICFRHHETSGSVPTDYQLQM 238
Db 180 HKVTLSSWYHRCWAKISNNMTFSGKLVNQDGFYLYLANICFRHHETSGDLATEYQLQM 239
QY 239 VYVTKTSIKIPSSHTLMKGGSTKYNWGNSEFHYFSINVGFFKLRSGEEISIEVSNPSLL 299
Db 240 VYVTKTSIKIPSSHTLMKGGSTKYNWGNSEFHYFSINVGFFKLRSGEEISIEVSNPSLL 299
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119 KQAFQAVOKELQHIYVGSQHIRAEKAMVDGSLDLAKSKLEQAQFAHLTINATDIPSGS 179
 179 HKVTLSSWYHNRGKAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLM 238
 180 HKVLSLSSWYHNRGKAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGDLATEYLQLM 239
 239 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIOVSNPSLL 298
 240 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIOVSNPSLL 299
 299 DPQDATYFAGKRVQDID 316
 300 DPQDATYFAGKRVQDID 317

RESULT 10

US-09-215-649A-13
 ; Sequence 13, Application US/09215649A
 ; Patent No. 6271349

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
 Galibert, Laurent
 Maraskovsky, Eugene
 TITLE OF INVENTION: Receptor Activator of NF-kappaB
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESS: Immunex Corporation, Law Department
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/215,649A
 FILING DATE: 17-Dec-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/996,139
 FILING DATE: <Unknown>
 APPLICATION NUMBER: USSN 08/813,509
 FILING DATE: 07 MARCH 1997
 APPLICATION NUMBER: USSN 08/772,330
 FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2851-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-215-649A-13

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
 Best Local Similarity 84.3%; Pred. No. 1.1e-131;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLRSGEEMSGGPGVPHGPHLPAPAPAPPPAAASRSMFVALLGLGQ 60
 DB 1 MRRASRDYTKYLRSGEEMSGGPGVPHGPHLPAPAPAPPPAAASRSMFVALLGLGQ 59

QY 61 VVCSIALFLYFRAQMDPNRISEDTCHFYRLRLHENAGLDSTLESDT--LPDSCRM 118
 DB 60 VVCSVALFFYFRAQMDPNRISEDTCHFYRLRLHENAGLDSTLESDT--LPDSCRM 119
 QY 119 KQAFQAVOKELQHIYVGSQHIRAEKAMVDGSLDLAKSKLEQAQFAHLTINATDIPSGS 178
 DB 120 KQAFQAVOKELQHIYVGSQHIRAEKAMVDGSLDLAKSKLEQAQFAHLTINATDIPSGS 179
 QY 179 HKVTLSSWYHNRGKAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLM 238
 DB 180 HKVLSLSSWYHNRGKAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGDLATEYLQLM 239
 QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIOVSNPSLL 298
 DB 240 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIOVSNPSLL 299
 QY 299 DPQDATYFAGKRVQDID 316
 DB 300 DPQDATYFAGKRVQDID 317

RESULT 11

US-09-052-521C-4
 ; Sequence 4, Application US/09052521C
 ; Patent No. 6316408

GENERAL INFORMATION:

APPLICANT: Boyle, William J.
 TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
 FILE REFERENCE: A-4518rv
 CURRENT APPLICATION NUMBER: US/09/052,521C
 CURRENT FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 08/880,855
 PRIOR FILING DATE: 1997-06-23
 PRIOR APPLICATION NUMBER: 08/842,842
 PRIOR FILING DATE: 1997-04-16
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 4
 LENGTH: 317
 TYPE: PRT
 ORGANISM: Human
 US-09-052-521C-4

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
 Best Local Similarity 84.3%; Pred. No. 1.1e-131;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLRSGEEMSGGPGVPHGPHLPAPAPAPPPAAASRSMFVALLGLGQ 60
 DB 1 MRRASRDYTKYLRSGEEMSGGPGVPHGPHLPAPAPAPPPAAASRSMFVALLGLGQ 59
 QY 61 VVCSIALFLYFRAQMDPNRISEDTCHFYRLRLHENAGLDSTLESDT--LPDSCRM 118
 DB 60 VVCSVALFFYFRAQMDPNRISEDTCHFYRLRLHENAGLDSTLESDT--LPDSCRM 119
 QY 119 KQAFQAVOKELQHIYVGSQHIRAEKAMVDGSLDLAKSKLEQAQFAHLTINATDIPSGS 178
 DB 120 KQAFQAVOKELQHIYVGSQHIRAEKAMVDGSLDLAKSKLEQAQFAHLTINATDIPSGS 179
 QY 179 HKVTLSSWYHNRGKAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLM 238
 DB 180 HKVLSLSSWYHNRGKAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGDLATEYLQLM 239
 QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIOVSNPSLL 298
 DB 240 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIOVSNPSLL 299
 QY 299 DPQDATYFAGKRVQDID 316
 DB 300 DPQDATYFAGKRVQDID 317

RESULT 12

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-354-2

Query Match 15.4%; Score 258.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred. No. 1.6e-17;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
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QY 101 QDSTLESEDTLPDCSRMRKQAFQGVOK-----ELOHIVGQRFSGAPAMM 146
DB 65 WDP--NDEESMNSPCQVQWQLRQVRKMLRTSEETISTVQEKQONISPL----- 113
QY 147 EGSWLDVAQGRKPEAOPFAHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS 196
DB 114 -----VRENGPQVRA--AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHFLS 165
QY 197 NMTLSNGKLVRNODGFYILYANICFRHHTSGSVPTDYILQLMWYVVKTSIKIPSSHNLAK 256
DB 166 NLHLRNGELVIHEKGFYIYSQTYFRPQOEIKENTNDQWQYIYKYT-SYDPDILLMK 224
QY 257 GGSTKNWGNSEPHFYISNVGGFFKLRAEIEISIQVSNPSLLDPDQDQATYFGAFV 312
DB 225 SARNSCWSKDAEYGLYSIYOGGIFELKENDRIEIVSVTNEHLIDMDHEASFFGAFV 280

RESULT 15
US-08-584-031-1
Sequence 1, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 15.4%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred. No. 1.6e-17;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
QY 43 PAASRSMFLALGLGIGVGVCSIALFLYFRAQMD--PNRISEDSSTHCYRILRLHENAGL 100
DB 10 PSIGQTCVLIVITVLLQSLCVAVTYVTFNELKQMDKYKSGIACF-----LKEDDSY 64
QY 101 QDSTLESEDTLPDCSRMRKQAFQGVOK-----ELOHIVGQRFSGAPAMM 146
DB 65 WDP--NDEESMNSPCQVQWQLRQVRKMLRTSEETISTVQEKQONISPL----- 113
QY 147 EGSWLDVAQGRKPEAOPFAHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS 196
DB 114 -----VRENGPQVRA--AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHFLS 165
QY 197 NMTLSNGKLVRNODGFYILYANICFRHHTSGSVPTDYILQLMWYVVKTSIKIPSSHNLAK 256
DB 166 NLHLRNGELVIHEKGFYIYSQTYFRPQOEIKENTNDQWQYIYKYT-SYDPDILLMK 224
QY 257 GGSTKNWGNSEPHFYISNVGGFFKLRAEIEISIQVSNPSLLDPDQDQATYFGAFV 312
DB 225 SARNSCWSKDAEYGLYSIYOGGIFELKENDRIEIVSVTNEHLIDMDHEASFFGAFV 280

Search completed: April 16, 2003, 12:21:16
Job time : 14.5 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:18:42 ; Search time 14.5 Seconds
(without alignments)
1647.861 Million cell updates/sec

Title: US-09-787-126-6
Perfect score: 1675
Sequence: 1 MRRASDYGYKLRSEMG.....LLDPQDQATYFGAKVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 288829 seqs, 7561385 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	9 US-10-017-910-4	Sequence 4, Appli
2	1675	100.0	316	9 US-10-105-057-2	Sequence 2, Appli
3	1554	92.8	294	9 US-09-877-650-11	Sequence 11, Appl
4	1554	92.8	294	10 US-09-871-856-11	Sequence 11, Appl
5	1417.5	84.6	317	9 US-09-877-650-13	Sequence 13, Appl
6	1417.5	84.6	317	10 US-09-813-329-7	Sequence 7, Appli
7	1417.5	84.6	317	10 US-09-871-856-13	Sequence 13, Appl
8	1101	65.7	245	9 US-10-017-910-2	Sequence 2, Appli
9	855	51.0	160	9 US-09-779-050A-14	Sequence 14, Appl
10	768	45.9	160	9 US-09-779-050A-15	Sequence 15, Appl
11	496	29.6	109	10 US-09-911-777-8	Sequence 8, Appli
12	238.5	15.4	279	12 US-10-066-209-3	Sequence 3, Appli
13	238.5	15.4	281	8 US-08-916-625B-6	Sequence 6, Appli
14	238.5	15.4	281	8 US-08-971-317A-8	Sequence 8, Appli
15	238.5	15.4	281	9 US-10-001-054-54	Sequence 54, Appl
16	238.5	15.4	281	9 US-10-093-766-54	Sequence 54, Appl
17	238.5	15.4	281	9 US-10-174-654-11	Sequence 11, Appl
18	238.5	15.4	281	9 US-10-151-882-41	Sequence 41, Appl
19	238.5	15.4	281	10 US-09-813-329-17	Sequence 17, Appl

20	258.5	15.4	281	10 US-09-193-663-8	Sequence 8, Appli
21	258.5	15.4	281	10 US-09-934-465-1	Sequence 1, Appli
22	258.5	15.4	281	12 US-10-039-785-66	Sequence 66, Appl
23	258.5	15.4	281	12 US-10-011-125-4	Sequence 4, Appli
24	244	14.6	291	9 US-10-017-910-6	Sequence 6, Appli
25	234	14.0	296	9 US-10-185-425-5	Sequence 5, Appli
26	232	13.9	246	10 US-09-855-544A-13	Sequence 13, Appl
27	230.5	13.8	168	10 US-09-900-530A-10	Sequence 10, Appl
28	229.5	13.7	166	9 US-09-779-050A-16	Sequence 16, Appl
29	225	13.4	172	9 US-09-779-050A-17	Sequence 17, Appl
30	220.5	13.2	164	12 US-10-116-378-29	Sequence 29, Appl
31	183	10.9	278	10 US-09-246-129B-6	Sequence 6, Appli
32	183	10.9	278	10 US-09-899-059-6	Sequence 6, Appli
33	182	10.9	279	9 US-10-017-910-5	Sequence 5, Appli
34	181	10.8	279	8 US-08-971-317A-4	Sequence 4, Appli
35	181	10.8	279	10 US-09-193-663-4	Sequence 4, Appli
36	176	10.5	87	10 US-09-880-457-4	Sequence 4, Appli
37	176	10.5	94	10 US-09-880-457-5	Sequence 5, Appli
38	176	10.5	95	9 US-10-237-884-82	Sequence 82, Appl
39	176	10.5	95	9 US-10-230-163-82	Sequence 82, Appl
40	176	10.5	95	9 US-10-218-631-82	Sequence 82, Appl
41	176	10.5	95	9 US-10-230-338-82	Sequence 82, Appl
42	176	10.5	95	9 US-10-230-414-82	Sequence 82, Appl
43	176	10.5	95	9 US-10-216-159A-82	Sequence 82, Appl
44	176	10.5	95	10 US-09-880-457-6	Sequence 6, Appli
45	173.5	10.4	281	8 US-08-971-317A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-017-910-4
; Sequence 4, Application US/10017910
; Patent No. US20020159970A1

GENERAL INFORMATION:

APPLICANT: Choi, Yongwon
Wong, Brian
Josien, Regis
Steinman, Ralph

TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY

INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/017,910

FILING DATE: 14-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/447,035

FILING DATE: 1999-11-22

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-200

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

QY	1	MRRASRDYGKYLRSSEEMSGPGVPHEGPHLPAPAPAPPAAASRSMFLALLGLGLGQ	60
Dd	1	MRRASRDYGKYLRSSEEMSGPGVPHEGPHLPAPAPAPPAAASRSMFLALLGLGLGQ	60
QY	61	VCSIALFLFRAQMOPNRISESTHCFYRIILRLHENAGLDSTLESDTLPDSCRMKQ	120
Dd	61	VCSIALFLFRAQMOPNRISESTHCFYRIILRLHENAGLDSTLESDTLPDSCRMKQ	120
QY	121	AFCGAVOKELQHIVGPORFGSAPAMWEGSWLDVAQRCKPEAQFAHLTTNAASIPSSGHK	180
Dd	121	AFCGAVOKELQHIVGPORFGSAPAMWEGSWLDVAQRCKPEAQFAHLTTNAASIPSSGHK	180
QY	181	VTLSWSYHDRGWAKISMTLSNGKLRYNQDPFYLYANICFRHHETSGSVPTDYQLMWY	240

Db 60 VVCSVALLFFYFRAQMDPNRISDSTHCHYRILRLHENADFDTLSESDTKLIPDSCRR 119
Qy 119 KOAFQAVOKELQHVGPQFSGAPAMGEGSWLDVAORQKPEAOPFAHLITNAASIPSGS 178
Db 120 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAOPFAHLITNATDIPSGS 179
Qy 179 HKVTLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLILYANICFRHETSGSVPTDYLQ 238
Db 180 HKVTLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLILYANICFRHETSGDLATYLQ 239
Qy 239 VYVKTSTIKIPSSHNLMKGGSTKWSGNSSEPHFYSINVGFFKLRAGEEISIQVSNPSLL 298
Db 240 VYVKTSTIKIPSSHNLMKGGSTKWSGNSSEPHFYSINVGFFKLRAGEEISIEVSNPSLL 299
Qy 299 DPQDQATYFGAFKVRDID 316
Db 300 DPQDQATYFGAFKVRDID 317

RESULT 6

US-09-813-329-7

Sequence 7, Application US/09813329

Patent No. US20020012968A1

GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-7

Query Match. 84.6%; Score 1417.5; DB 10; Length 317;
Best Local Similarity 84.3%; Pred. No. 5,2e-117;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYKYLRSSEEMSGGPGVPHGPHLPAPAPAPPPAASRSMFALLGLGLGQ 60
Db 1 MRRASRDYKYLRSSEEMSGGPGVPHGPHLPAPAPPPAASRSMFALLGLGLGQ 59
Qy 61 VVCSVALLFFYFRAQMDPNRISDSTHCHYRILRLHENADFDTLSESDTKLIPDSCRR 118
Db 60 VVCSVALLFFYFRAQMDPNRISDSTHCHYRILRLHENADFDTLSESDTKLIPDSCRR 119
Qy 119 KOAFQAVOKELQHVGPQFSGAPAMGEGSWLDVAORQKPEAOPFAHLITNAASIPSGS 178
Db 120 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAOPFAHLITNATDIPSGS 179
Qy 179 HKVTLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLILYANICFRHETSGSVPTDYLQ 238
Db 180 HKVTLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLILYANICFRHETSGDLATYLQ 239
Qy 239 VYVKTSTIKIPSSHNLMKGGSTKWSGNSSEPHFYSINVGFFKLRAGEEISIQVSNPSLL 298
Db 240 VYVKTSTIKIPSSHNLMKGGSTKWSGNSSEPHFYSINVGFFKLRAGEEISIEVSNPSLL 299
Qy 299 DPQDQATYFGAFKVRDID 316
Db 300 DPQDQATYFGAFKVRDID 317

RESULT 7

US-09-871-856-13

Sequence 13, Application US/09871856

Patent No. US20020081720A1

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER/READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-856-13

Query Match 84.6%; Score 1417.5; DB 10; Length 317;
Best Local Similarity 84.3%; Pred. No. 5,2e-117;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYKYLRSSEEMSGGPGVPHGPHLPAPAPPPAASRSMFALLGLGLGQ 60
Db 1 MRRASRDYKYLRSSEEMSGGPGVPHGPHLPAPAPPPAASRSMFALLGLGLGQ 59
Qy 61 VVCSVALLFFYFRAQMDPNRISDSTHCHYRILRLHENADFDTLSESDTKLIPDSCRR 118
Db 60 VVCSVALLFFYFRAQMDPNRISDSTHCHYRILRLHENADFDTLSESDTKLIPDSCRR 119
Qy 119 KOAFQAVOKELQHVGPQFSGAPAMGEGSWLDVAORQKPEAOPFAHLITNAASIPSGS 178
Db 120 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAOPFAHLITNATDIPSGS 179
Qy 179 HKVTLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLILYANICFRHETSGSVPTDYLQ 238
Db 180 HKVTLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLILYANICFRHETSGDLATYLQ 239
Qy 239 VYVKTSTIKIPSSHNLMKGGSTKWSGNSSEPHFYSINVGFFKLRAGEEISIQVSNPSLL 298
Db 240 VYVKTSTIKIPSSHNLMKGGSTKWSGNSSEPHFYSINVGFFKLRAGEEISIEVSNPSLL 299
Qy 299 DPQDQATYFGAFKVRDID 316
Db 300 DPQDQATYFGAFKVRDID 317

RESULT 8

US-10-017-910-2
; Sequence 2, Application US/10017910
; Patent No. US20020159970A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; Wong, Brian
; Josien, Regis
; Steinman, Ralph
; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SA
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/017,910
; FILING DATE: 14-Dec-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/447,035
; FILING DATE: 1999-11-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 245 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-017-910-2

Query Match 65.7%; Score 1101; DB 9; Length 245;
Best Local Similarity 84.1%; Pred. No. 2.7e-89;
Matches 206; Conservative 14; Mismatches 23; Indels 2; Gaps 1;
QY 74 QMDPNRISDSTHCFFYRILRHENAGLDSTLESDT--LPDSRRMKQAFQGAQVQKELQ 131
Db 1 QMDPNRISDSTHCFFYRILRHENAGLDSTLESDT--LPDSRRMKQAFQGAQVQKELQ 60
QY 132 HIVGPQFSGAPNMGCSWLDVAQRGPEAQPFAHLTINAAIPSGSHKVTLSWYHDG 191
Db 61 HIVGSHIRAEKAVDGSWLDLAKRSKLEAQPFAHLTINAAIPSGSHKVTLSWYHDG 120
QY 192 WAKLSNMTLSNGLRVNQDGFYILYANICFRHETSGSVPTDYQLQVMVYVVKTSIKIPSS 251
Db 121 WAKLSNMTLSNGLRVNQDGFYILYANICFRHETSGSVPTDYQLQVMVYVVKTSIKIPSS 180
QY 252 HNLKMGSTKNWGSNPFHYSINVGGFFKLKRGAGEEISIQVSNPDLDPDQDATYFGAFK 311
Db 181 HNLKMGSTKNWGSNPFHYSINVGGFFKLKRGAGEEISIEVSNPDLDPDQDATYFGAFK 240
QY 312 VQDID 316
Db 241 VRDID 245

RESULT 9

US-09-779-050A-14
; Sequence 14, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-779-050A-14

Query Match 51.0%; Score 855; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 7e-68;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKPEAOPFAHLTINAAIPSGSHKVTLSWYHDGWAQKISNMTLSNGLRVNQDGFYLY 216
Db 1 GKPEAOPFAHLTINAAIPSGSHKVTLSWYHDGWAQKISNMTLSNGLRVNQDGFYLY 60
QY 217 ANICFRHETSGSVPTDYQLQVMVYVVKTSIKIPSSHNLKMGSTKNWGSNPFHYSINV 276
Db 61 ANICFRHETSGSVPTDYQLQVMVYVVKTSIKIPSSHNLKMGSTKNWGSNPFHYSINV 120
QY 277 GGFFKLKRGAGEEISIQVSNPDLDPDQDATYFGAFKVQDID 316
Db 121 GGFFKLKRGAGEEISIQVSNPDLDPDQDATYFGAFKVQDID 160

RESULT 10

US-09-779-050A-15
; Sequence 15, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-779-050A-15

Query Match 45.9%; Score 768; DB 9; Length 160;
Best Local Similarity 89.9%; Pred. No. 3.2e-60;
Matches 143; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 158 KPEAOPFAHLTINAAIPSGSHKVTLSWYHDGWAQKISNMTLSNGLRVNQDGFYLYA 217
Db 2 KLEAOPFAHLTINATDIPSGSHKVTLSWYHDGWAQKISNMTLSNGLRVNQDGFYLYA 61
QY 218 NICFRHETSGSVPTDYQLQVMVYVVKTSIKIPSSHNLKMGSTKNWGSNPFHYSINV 277
Db 62 NICFRHETSGDLATEYLQVMVYVVKTSIKIPSSHTLMKGGSTKNWGSNPFHYSINV 121


```

; . SEQUENCE CHARACTERISTICS:
; . LENGTH: 281 amino acids
; . TYPE: amino acid
; . STRANDEDNESS: single
; . TOPOLOGY: linear
; . MOLECULE TYPE: protein
US-08-916-G25B-6

```

```

Query Match      15.4%; Score 258.5; DB 8; Length 281;
Best Local Similarity 26.4%; Pred. No. 5e-15;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

QY 43 PAASRSFIALLLGIGLQGVCSIALFLYFRAQMD--PNRISESTHCFYRLRLHENAGL 100
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 PSLGQTCVLIVIFVLQSLCAVTVYFYTNELKQMDKYSKGIACF-----LKEDDSY 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 101 QDSTLESEDTLPDSCRMKQAFQAVOK-----ELQHLVGPQRFSGAPAMM 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
b 65 WDP--NDEESNNSPCWQKWLQQLVRKMLRSEETISIVQEKQKINSL----- 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 EGSWLDAVAQKGEPAQFFAHLT-----INAAISPGSHKVTL-----SSWHDR-GWAKIS 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 -----VREGPQRYA--AHITGRGSNTLSPNSKNEALGRKINSWESSRGHSFLS 165
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 197 NMTLSNGKLVRNODGFYLLYANICFRHETSGSVPTDYLQLMVTYVVKTSIKIPSSHLMK 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 166 NLHLRNGELVIERKGFYYIYSQTVFRQEIEKENTKNDKQMVYIYKVT-SYDPILLMK 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 257 GGSTKNWNSNEPHFYISYNGVGFKKLAGEEISIQVNSPLLDPPQDQATVFGAFKV 312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 SARNSKSDAETGLYSIOGIFELKENDRIFYSVTNEHLMDHDEASFGAPLV 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 14
US-08-971-317A-8
; Sequence 8, Application US/08971317A
; Patent No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Willey, Steven R.
; TITLE OF INVENTION: TNF-DELTA LI
; TITLE OF INVENTION: TNF-DELTA LI
; NUMBER OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mini C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid

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```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. US2
US-08-971-317A-8

```

[illegible]

RESULT 15
US-10-001-054-54
Sequence 54, Application US/10001054
Publication No. US20020192209A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Baker, Kevin
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Hebert, Carolyn
APPLICANT: Heuzel, William
APPLICANT: Keuzekoff, Rhona
APPLICANT: Shelton, David
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FOR THE TREATMENT OF CELL GROWTH
FILE REFERENCE: P3034R1PCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/075920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/096891
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/096894
PRIOR FILING DATE: 1998-08-17

;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/100263
;; PRIOR FILING DATE: 1998-09-14
;; PRIOR APPLICATION NUMBER: 60/100390
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/101476
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/107783
;; PRIOR FILING DATE: 1998-11-10
;; PRIOR APPLICATION NUMBER: 60/108849
;; PRIOR FILING DATE: 1998-11-18
;; PRIOR APPLICATION NUMBER: 60/112420
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113296
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/115554
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/116533
;; PRIOR FILING DATE: 1999-01-20
;; PRIOR APPLICATION NUMBER: 60/123618
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: 60/131294
;; PRIOR FILING DATE: 1999-04-07
;; PRIOR APPLICATION NUMBER: 60/140650
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/162506
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: 60/170262
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/187202
;; PRIOR FILING DATE: 2000-03-03
;; PRIOR APPLICATION NUMBER: 60/209832
;; PRIOR FILING DATE: 2000-06-05
;; PRIOR APPLICATION NUMBER: 60/232887
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 09/180997
;; PRIOR FILING DATE: 1998-11-19
;; PRIOR APPLICATION NUMBER: 09/218517
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 09/284291
;; PRIOR FILING DATE: 1999-04-12
;; PRIOR APPLICATION NUMBER: 09/380137
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380913
;; PRIOR FILING DATE: 1999-09-09
;; PRIOR APPLICATION NUMBER: 09/403297
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/423741
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: 09/709238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/866034
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 09/872035
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/882636
;; PRIOR FILING DATE: 2001-06-14
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 09/924419
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: 09/927796
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: 09/929404
;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 09/941992
;; PRIOR FILING DATE: 2001-08-28
;; PRIOR APPLICATION NUMBER: 09/946374
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: PCT/US98/18824
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/US99/00106
;; PRIOR FILING DATE: 1999-01-05
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: PCT/US99/08615
;; PRIOR FILING DATE: 1999-04-20
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/20111
;; PRIOR FILING DATE: 1999-09-01
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28551
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28634
;; PRIOR FILING DATE: 1999-12-01
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00376
;; PRIOR FILING DATE: 2000-01-06
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: PCT/US00/04341
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/04342
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: PCT/US00/06884
;; PRIOR FILING DATE: 2000-03-15
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: PCT/US00/13705
;; PRIOR FILING DATE: 2000-05-17
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: PCT/US00/14941
;; PRIOR FILING DATE: 2000-05-30
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US00/22031
;; PRIOR FILING DATE: 2000-08-11
;; PRIOR APPLICATION NUMBER: PCT/US00/23522
;; PRIOR FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: PCT/US00/30873
;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: PCT/US01/06666
;; PRIOR FILING DATE: 2001-03-01
;; PRIOR APPLICATION NUMBER: PCT/US01/17092
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29

;; PRIOR APPLICATION NUMBER: PCT/US01/21735
 ;; PRIOR FILING DATE: 2001-07-09
 ;; PRIOR APPLICATION NUMBER: PCT/US01/27099
 ;; PRIOR FILING DATE: 2001-08-29
 ;; NUMBER OF SEQ ID NOS: 91
 ;; SEQ ID NO 54
 ;; LENGTH: 281
 ;; TYPE: PRT
 ;; ORGANISM: Homo Sapien
 US-10-001-054-54

Query Match 15.48; Score 258.5; DB 9; Length 281;
 Best Local Similarity 26.48; Pred. No. 5e-15; Indels 51; Gaps 10;
 Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

Qy	43	PAASRSMFLALIGLIGQVVGCSIALFLYFRAQMD--PNRISEDSHCHFYRILRLHENAGL	100
Db	10	PSLGQTCVLIYFTVLQSLCAVTVYFTNELKQMDKYSKGIACF-----LKEDDSY	64
y	101	QDSTLESDTLPDSCRRMKQAFQGAQVK-----ELQHVGPQRFSGAPAMM	146
Db	65	WDP--NDESNMSPCQWKQLRQLVRKMLRTSEETISTVQEKQONISPL-----	113
Qy	147	EGSWLDVAQRGKPEAQPFahlT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS	196
Db	114	-----VRERGQPRVA--AHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFLS	165
Qy	197	NMTLSNGKLRVNODGFYLYANICFRHHETSGSVPTDYQLMAYVYVVKTSIKIPSSHNLMK	256
Db	166	NHLRNGELVTHEKGFYIYSQTYFRQEEIKENTKQKQVQYIYKYT-SYDPDILLMK	224
Qy	257	GGSTKNWGSNSEFFHYSINVGGFFKLRAEEISIQVSNPSLLDDPDODATYFGAFKV	312
Db	225	SARNSCWKSQDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV	280

Search completed: April 16, 2003, 12:21:52
 Job time : 15.5 secs